

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 24, 2006, 08:55:09 ; Search time 18 Seconds
(without alignments)
291.129 Million cell updates/sec

Title: US-09-978-360A-437

Perfect score: 1831

Sequence: 1 MESGRPSLCQFILGTTVS.....PKKPCICQALTRVPLVNS 352

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 117670 seqs, 14887254 residues

117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.rep:*
2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.rep:*
3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.rep:*
4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.rep:*
5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.rep:*
6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.rep:*
7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.rep:*
8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.rep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result- No.	Score	Match	Query Length	DB ID	Description
1	1831	100.0	352	US-09-978-360A-437	Sequence 437, App
2	155.5	8.5	723	US-11-072-512-2572	Sequence 2572, App
3	143.5	7.8	363	US-11-072-512-3425	Sequence 3425, App
4	112	6.1	795	US-11-072-512-2378	Sequence 2378, App
5	107	5.8	593	US-11-169-041-239	Sequence 239, App
6	107	5.8	619	US-11-072-512-2497	Sequence 2497, App
7	99	5.4	843	US-11-072-512-2043	Sequence 2043, App
8	98.5	5.4	149	US-11-226-657-205	Sequence 205, App
9	98.5	5.4	166	US-11-226-657-204	Sequence 204, App
10	98.5	5.4	355	US-11-135-855-44	Sequence 44, App
11	98.5	5.4	491	US-11-069-642-137	Sequence 137, App
12	98	5.4	203	US-11-024-959-509	Sequence 509, App
13	97	5.3	574	US-10-821-234-1654	Sequence 1654, App
14	95.5	5.2	645	US-11-072-512-2588	Sequence 2588, App
15	93.5	5.1	670	US-11-072-512-2035	Sequence 2035, App
16	93	5.1	810	US-09-978-360A-712	Sequence 712, App
17	92	5.0	916	US-10-467-657-4242	Sequence 4242, App
18	90	4.9	610	US-11-072-512-2672	Sequence 2672, App
19	89.5	4.9	328	US-11-024-959-517	Sequence 517, App
20	89.5	4.9	468	US-11-072-512-3654	Sequence 3654, App
21	89	4.9	2036	US-11-124-368A-276	Sequence 276, App
22	89	4.9	2036	US-11-124-368A-280	Sequence 280, App
23	89	4.9	2036	US-11-124-368A-281	Sequence 281, App
24	89	4.9	2044	US-11-124-368A-278	Sequence 278, App
25	89	4.9	2144	US-11-124-368A-277	Sequence 277, App

ALIGNMENTS

26	87	4.8	664	7	US-11-124-367A-439	Sequence 439, App
27	87	4.8	667	7	US-11-124-367A-440	Sequence 440, App
28	86	4.7	360	6	US-10-834-397-293	Sequence 293, App
29	86	4.7	360	7	US-11-165-067A-26	Sequence 26, App
30	85.5	4.7	262	7	US-11-072-512-2104	Sequence 2104, App
31	83.5	4.6	451	7	US-11-054-168B-6	Sequence 6, App
32	83	4.5	381	6	US-10-517-939-326	Sequence 326, App
33	82.5	4.5	306	7	US-11-074-176-290	Sequence 290, App
34	82.5	4.5	421	7	US-11-098-686-10798	Sequence 10798, App
35	82.5	4.5	2630	7	US-11-186-731-2	Sequence 2, App
36	82.5	4.5	7968	7	US-11-186-731-5	Sequence 5, App
37	81.5	4.5	648	6	US-10-793-626-568	Sequence 568, App
38	81.5	4.5	4384	6	US-10-821-234-1120	Sequence 1120, App
39	81	4.4	1165	7	US-11-197-380-6	Sequence 6, App
40	81	4.4	1482	7	US-11-181-330-2	Sequence 2, App
41	80.5	4.4	430	7	US-11-098-686-11038	Sequence 11038, App
42	80.5	4.4	471	7	US-11-072-512-3482	Sequence 3482, App
43	80.5	4.4	547	6	US-10-177-412-2	Sequence 2, App
44	80.5	4.4	816	7	US-11-072-512-2341	Sequence 2341, App
45	80.5	4.4	8746	7	US-11-098-686-10232	Sequence 10232, App

RESULT 1
US-09-978-360A-437
Sequence 437, Application US/09978360A
Publication No. US20060009633A9
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste Dumas Milne
APPLICANT: Bouguetier, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56 US4.CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR FILING DATE: -03-04
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1999-02-09
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent.pm
SEQ ID NO 437
LENGTH: 352
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 23..-1
US-09-978-360A-437
Query Match 100.0%; Score 1831; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.4e-154;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGGRBPLCOFILIGTTSVTTAALYSYTRKARVSOELKAKVHLGEDIKSLISBAPG 60
 Db 1 MESGGRBPLCOFILIGTTSVTTAALYSYTRKARVSOELKAKVHLGEDIKSLISBAPG 60

QY 61 KCVPAVAVEGAVRSVKETLINSQFVENCCKVYQRLTLOEHKMMVNRTHLWNDCKSLIHOR 120
 Db 61 KCVPAVAVEGAVRSVKETLINSQFVENCCKVYQRLTLOEHKMMVNRTHLWNDCKSLIHOR 120

QY 121 TMTVPFDLVPHEGDVDVAVRVLKPLDSVDLGLFTVYKFPHSISQFTDVI GHYISGERPK 180
 Db 121 TMTVPFDLVPHEGDVDVAVRVLKPLDSVDLGLFTVYKFPHSISQFTDVI GHYISGERPK 180

QY 181 GIOETEBELKVAGATLTGVELVLNNSVRLQPPKQMOYVILSSODPESLLORESSVRLW 240
 Db 181 GIOETEBELKVAGATLTGVELVLNNSVRLQPPKQMOYVILSSODPESLLORESSVRLW 240

QY 241 KVALVFGFATCATLFFILRKQYLQROERLRLKQMOEFQHEAQLLSRAKPEDRESLKS 300
 Db 241 KVALVFGFATCATLFFILRKQYLQROERLRLKQMOEFQHEAQLLSRAKPEDRESLKS 300

QY 301 ACVCLSSFKSCVFLBEGHVCSTECYRALPEPKKCPICQOATRVIPLYNS 352
 Db 301 ACVCLSSFKSCVFLBEGHVCSTECYRALPEPKKCPICQOATRVIPLYNS 352

RESULT 2

US-11-072-512-2572
 ; Sequence 2572, Application US/11072512
 ; Publication No. US20060029945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: MAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOHITO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOKUJI
 ; APPLICANT: NAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: 084335-0191
 ; CURRENT APPLICATION NUMBER: US/11/072,512
 ; PRIOR FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: US 60/350,978
 ; PRIOR FILING DATE: 2002-01-25
 ; PRIOR APPLICATION NUMBER: JP 2001-379298
 ; PRIOR FILING DATE: 2001-11-05
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2572
 ; LENGTH: 723
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-072-512-2572

Query Match

Best Local Similarity 34.3%; Pred. No. 8.5e-06;
 Matches 37; Conservative 16; Mismatches 38; Indels 17; Gaps 3;

QY 259 LRKQYIQRQERIRLKQMOEEF-----QEHRAQLLSRAKPEDRESLSACV 304
 Db 618 LRHEILRRVQELIDARIQBELKPPMGGEVVTPTAPQEPESVRSPAPAELEVAQSECV 677

QY 305 CLSSFKSCVFLBEGHVCSTECYRALPEPKKCPICQOATRVIPLYNS 352
 Db 678 CLERAQMFIFMGHVCCEGQCCQPL---RTPEPLCRQDLAQRLRIYHS 722

RESULT 3

US-11-072-512-3425
 ; Sequence 3425, Application US/11072512
 ; Publication No. US20060029945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: MAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOHITO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOKUJI
 ; APPLICANT: NAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: 084335-0191
 ; CURRENT APPLICATION NUMBER: US/11/072,512
 ; PRIOR FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: US 60/350,978
 ; PRIOR FILING DATE: 2002-01-25
 ; PRIOR APPLICATION NUMBER: JP 2001-379298
 ; PRIOR FILING DATE: 2001-11-05
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3425
 ; LENGTH: 363
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-072-512-3425

Query Match

Best Local Similarity 7.8%; Score 143.5; DB 7; Length 363;
 Matches 41; Conservative 28; Mismatches 40; Indels 27; Gaps 7;

QY 224 QFDBLLQROESSVRLMWKVALVF-GFATCATLFFILRKQYLQROERLRLKQMOEFQ 281
 Db 248 EDIBGLTVRQ-----LKEIILARNFVNYKGCCKEKLW-----ERYTRLXKQKGLQ 293

QY 282 HBAQLLSRAKPEDRESLSKA-----CVCLSSFKSCVFLBEGHVCSTECYRALPEPKK 336
 Db 294 ---HLVSGAEDQNGAVVSGLEENLCKICMDSPIQVILBEGHVTCTCKCKRNN---C 347

QY 337 PICRQATRVIPLYNS 352
 Db 348 PICRQYIRAVHVERS 363

RESULT 4

US-11-072-512-2378
 ; Sequence 2378, Application US/11072512
 ; Publication No. US20060029945A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: MAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO

```

; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT FILING DATE: 2005-03-07
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2378
; LENGTH: 795
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2378

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Query Match      6.1%; Score 112; DB 7; Length 795;
Best Local Similarity 35.9%; Pred. No. 0.068;
Matches 23; Conservative 9; Mismatches 22; Indels 10; Gaps 2;

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QY 285 QLSAKEDNESLKSACVCLSSFKSCVFLGCGVSCCTEYRALPEPKKCPICRQAIT 344
DB 645 QVQSTKIE-----CVCSDKKAVALFQCGHCAECENANLM---KKCVCRAYVE 694

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QY 345 RVIP 348
DB 695 RRVF 698

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RESULT 5
US-11-169-041-239
; Sequence 239, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT FILING DATE: 2005-06-28
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,405
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-239

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Query Match      5.8%; Score 107; DB 7; Length 593;
Best Local Similarity 46.0%; Pred. No. 0.12;
Matches 23; Conservative 4; Mismatches 21; Indels 2; Gaps 2;

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QY 293 EDRSLKSA-CVCLSSFKSCVFLGCGVSCCTEYRALP-EPKKCPICR 340
DB 181 EDEVSDNSAEVCVCLSDVADTLILPCRHLCLCNTCADTLRYQANNCPICR 230

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RESULT 6
US-11-072-512-2497
; Sequence 2497, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT FILING DATE: 2005-03-07
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2497
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2497

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Query Match      5.8%; Score 107; DB 7; Length 619;
Best Local Similarity 46.0%; Pred. No. 0.13;
Matches 23; Conservative 4; Mismatches 21; Indels 2; Gaps 2;

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QY 293 EDRSLKSA-CVCLSSFKSCVFLGCGVSCCTEYRALP-EPKKCPICR 340
DB 229 EDEVSDNSAEVCVCLSDVADTLILPCRHLCLCNTCADTLRYQANNCPICR 278

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RESULT 7
US-11-072-512-2043
; Sequence 2043, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191

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; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2043
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2043

Query Match      5.4%; Score 99; DB 7; Length 843;
Best Local Similarity 19.9%; Pred. No. 1;
Matches 88; Conservative 46; Mismatches 146; Indels 162; Gaps 19;

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QY 23 AALSYVRQKARVSOELKGAKKVH/GEDLKSILSEAPGK--CVPYAVIEGAVRSVKETLN 80
DB 430 AAILAKHFDARI-----VGTDIRSLMQLALASYVCYPH-----SLRAVERIPE 473
QY 81 SQFENCKGVQRLTQHKAVNRRT-----THLMNDC----- 113
DB 474 EQRI-----AMVRNLAPYEQRPMAQTWIIIVRLRFGCGFYRYRLPHLTKLEDANLP 529
QY 114 -----SKTHORTNTPFDLVPHEDGVAVAVLKPLDSYDLGETVEYKHPISQSF 166
DB 530 SLOKPCSTLLQOM-----ADLL--QQGPVAPSF--LMSVNLQMLWAPSEFTGMIOET 580
QY 167 TDVIGHYISGERPKGIQETEMLVGA-----TLTVGEBVLNNSVRLQ 211
DB 581 QQ-----AAERLERNFVDSRQLKVCATCFDLSVSLRVLEMITLIVPEIFLD-----WT 629
QY 212 PPKGMQVYLLSQPDFLLOQES-----SYRLMKVTLAVTFG----- 249
DB 630 RPTSEMLRLRLQNLNQVLRVTAERNLFDREVTLRLPLGESVDHPILVAVGIIVQL 689
QY 250 -----ATCATL--FFILRK-----QYLD 265
DB 690 VRGPASREQATSVLLADPCFQLRISICYLIGQEPBPAPGALAPDRKRSLOSVDYLS 749
QY 266 ROERLRKQKQOEFOHEAQLLSRAKPEDRESISKACVCLSGSPKSCVPLECGHVSCTE 325
DB 750 ADELAQVEQMLAH/LSASAQAAASLPTSEDL--CPICVAPHSVAFPGCHK-SCKA 805
QY 326 CY-RALPEPKKCPICRAITRV 346
DB 806 CINOHLMNNKDCFFCKTTIVSV 827

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```

RESULT 8
US-11-226-657-205
; Sequence 205, Application US/11226657
; Publication No. US20060025574A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006G13APIC1D2
; CURRENT APPLICATION NUMBER: US/11/226,657
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: 10/062,831
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/US98/10868
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: 1997-05-30

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; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: 1997-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 205
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-226-657-205

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```

Query Match      5.4%; Score 98.5; DB 7; Length 149;
Best Local Similarity 36.4%; Pred. No. 0.092;
Matches 20; Conservative 10; Mismatches 18; Indels 7; Gaps 3;

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```

QY 302 CVCLSSEFKSCVPLECGHVSCTEC-----YRALPEPKKCPICRAITRV--VIPLY 350
DB 13 CNICLETAREAVVSCGHL-YCWPCLHQWLETRPERQECVPCKAGISREKVVPLY 66

```

```

RESULT 9
US-11-226-657-204
; Sequence 204, Application US/11226657
; Publication No. US20060025574A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006G13APIC1D2
; CURRENT APPLICATION NUMBER: US/11/226,657
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: 10/062,831
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/US98/10868
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,356
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 204
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-226-657-204

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Query Match      5.4%; Score 98.5; DB 7; Length 166;
Best Local Similarity 36.4%; Pred. No. 0.11;
Matches 20; Conservative 10; Mismatches 18; Indels 7; Gaps 3;

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QY 302 CVCLSSEFKSCVPLECGHVSCTEC-----YRALPEPKKCPICRAITRV--VIPLY 350
DB 13 CNICLETAREAVVSCGHL-YCWPCLHQWLETRPERQECVPCKAGISREKVVPLY 66

```

RESULT 10
US-11-135-855-44
Sequence 44, Application US/11135855
Publication No. US2005025557A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.L.C.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50013
CURRENT APPLICATION NUMBER: US/11/135,855
CURRENT FILING DATE: 2005-05-24
PRIOR APPLICATION NUMBER: US/10/203,708
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FaetsEQ for Windows Version 3.0
SEQ ID NO 44
LENGTH: 355
TYPE: PRT
ORGANISM: Homo sapiens
US-11-135-855-44

Query Match 5.4%; Score 98.5; DB 7; Length 355;
Best Local Similarity 42.6%; Pred. No. 0.33;
Matches 26; Conservative 5; Mismatches 19; Indels 11; Gaps 4;
QY 283 EAOILSRAPKPEDEBSLSKACVCLSPKSCVPLECGHVCSTECTRALEPPKPCICROA 342
DB 297 EAOILSRAPKPEDEBSLSKACVCLSPKSCVPLECGHVCSTECTRALEPPKPCICROA 345
QY 343 I 343
DB 346 V 346

RESULT 11
US-11-069-642-137
Sequence 137, Application US/11069642
Publication No. US20050260626A1
GENERAL INFORMATION:
APPLICANT: LORENS, JAMES B.
APPLICANT: PRAY, TODD R.
APPLICANT: KINSELLA, TODD M.
APPLICANT: BENNETT, MARK K.
TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
FILE REFERENCE: RIGI-022CIP3
CURRENT APPLICATION NUMBER: US/11/069,642
CURRENT FILING DATE: 2005-02-28
PRIOR APPLICATION NUMBER: 10/232,758
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 10/422,536
PRIOR FILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 09/800,770
PRIOR FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: 60/187,130
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 168
SOFTWARE: PatentIn version 3.2
SEQ ID NO 137
LENGTH: 491
TYPE: PRT
ORGANISM: Homo sapiens
US-11-069-642-137

Query Match 5.4%; Score 98.5; DB 7; Length 491;
Best Local Similarity 31.0%; Pred. No. 0.53;

Matches 27; Conservative 18; Mismatches 25; Indels 17; Gaps 5;
QY 276 QEEFHEHAQLSRAPKPEDEBSLSKACVCLSPKSCVPLECGHVCSTECTRALEPPKPCICROA 324
DB 408 QEDVAFEF-----REETDKESEVSSSLPLNAIEPCVICGRPNKGCTVHGKTHLMACF 462
QY 325 ECVRALPEPKK-CPICROAIVTPIPLY 350
DB 463 TCARKLKKRKNKPCVPCROPIOMIVILTY 489

RESULT 12
US-11-024-959-509
Sequence 509, Application US/11024959
Publication No. US20060010516A1
GENERAL INFORMATION:
APPLICANT: FORSTER, RICHARD L.
APPLICANT: CONNETT, MARIE B.
APPLICANT: EMERSON, SARAH JANE
APPLICANT: GRIGOR, MURRAY ROBERT
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: LUND, STEVEN TROY
APPLICANT: MAGUSIN, ANDREAS
APPLICANT: KODRZYCKI, BOB
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 782
SOFTWARE: PatentIn version 3.3
SEQ ID NO 509
LENGTH: 203
TYPE: PRT
ORGANISM: Pinus radiata
US-11-024-959-509

Query Match 5.4%; Score 98; DB 7; Length 203;
Best Local Similarity 31.0%; Pred. No. 0.16;
Matches 22; Conservative 16; Mismatches 29; Indels 4; Gaps 3;
QY 285 QLSRAKPEDEBSLSKACVCLSPKSCVPLECGHVCSTECTRALEPPKPCICROA 341
DB 130 QLSRVQSDSEKVELTALICISTWEERTSTICGHI-FCKKCTINAHMKPCICROA 188
QY 342 AITRVIPLYNS 352
DB 189 AINNIHRIYIS 199

RESULT 13
US-10-821-234-1624
Sequence 1624, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crafin, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PC_SEQ_genes Version 1.0
SEQ ID NO 1624
LENGTH: 574
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1624

Query Match 5.3%; Score 97; DB 6; Length 574;
 Best Local Similarity 37.5%; Pred. No. 0.9;
 Matches 21; Conservative 4; Mismatches 23; Indels 8; Gaps 2;

QY 302 CVCCLSSFKSCVFLGHCVCCTECYRALPEPK-----CPICROAITRYIPLYNS 352
 DB 521 CTTCYEAHVDTVITGCMCLCYACGLRL---KKAHACCPICRPIKDIITKYRS 573

RESULT 14

US-11-072-512-2588
 ; Sequence 2588, Application US/11072512
 ; Publication No. US20060029945A1

GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOHITO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTYUKI
 ; APPLICANT: NAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: 08435-0191
 ; CURRENT APPLICATION NUMBER: US/11/072,512
 ; PRIOR FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: US 60/350,978
 ; PRIOR FILING DATE: 2002-01-25
 ; PRIOR APPLICATION NUMBER: JP 2001-379298
 ; PRIOR FILING DATE: 2001-11-05
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2588
 ; LENGTH: 645
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-072-512-2588

Query Match 5.2%; Score 95.5; DB 7; Length 645;
 Best Local Similarity 33.3%; Pred. No. 1.4;
 Matches 26; Conservative 9; Mismatches 28; Indels 15; Gaps 4;

QY 273 KQOEFOEHAQLLSRAKEDRESLSKACVCLSSFKSCVFLGHCVCCTECYRALPE 332
 DB 582 RQVEELOSRYRQMEERI-----TCPICIDSHIRLVF-QCGH-GACAPCGSAL-- 627
 QY 333 PKCPIROAITRYIPLY 350
 DB 628 -SACPICROPTRIDRIOTIF 644

RESULT 15

US-11-072-512-2035
 ; Sequence 2035, Application US/11072512
 ; Publication No. US20060029945A1

GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO

APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: IRIE, RYOTARO
 ; APPLICANT: TAMECHIKA, ICHIRO
 ; APPLICANT: SEKI, NAOHITO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTYUKI
 ; APPLICANT: NAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: Novel full length cDNA
 ; FILE REFERENCE: 08435-0191
 ; CURRENT APPLICATION NUMBER: US/11/072,512
 ; PRIOR FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: US 60/350,978
 ; PRIOR FILING DATE: 2002-01-25
 ; PRIOR APPLICATION NUMBER: JP 2001-379298
 ; PRIOR FILING DATE: 2001-11-05
 ; NUMBER OF SEQ ID NOS: 4096
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2035
 ; LENGTH: 670
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-072-512-2035

Query Match 5.1%; Score 93.5; DB 7; Length 670;
 Best Local Similarity 31.5%; Pred. No. 2.3;
 Matches 23; Conservative 13; Mismatches 28; Indels 9; Gaps 2;

QY 275 MOEFOEHAQLLSRAKEDRESLSKACVCLSSFKSCVFLGHCVCCTECYRALPEPK 334
 DB 109 LPEEERBEPLVFA-----EOPSVLCCQLCCSVFKDPVITTCGH---TEFCRCALKSE 159
 QY 335 KCPICROAITRYI 347
 DB 160 KCPVNVKLTIVV 172

Search completed: February 24, 2006, 08:58:09
 Job time : 19 secs

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OM protein - protein search, using sw model

Run on: February 24, 2006, 08:54:49 ; Search time 164 Seconds
(without alignments)
896.804 Million cell updates/sec

Title: US-09-978-360A-437
Perfect score: 1831
Sequence: 1 MESSGRPSLCFILGTSV.....PKKCPICQATRVIPLYNS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1831	100.0	352	US-09-978-360A-437	Sequence 437, App
2	1831	100.0	352	US-10-024-298A-75	Sequence 75, App1
3	1831	100.0	352	US-10-042-211A-75	Sequence 75, App1
4	1831	100.0	352	US-10-315-66A-105	Sequence 105, App
5	1831	100.0	352	US-10-221-62S-25	Sequence 25, App1
6	1831	100.0	352	US-10-169-39S-92	Sequence 92, App1
7	1831	100.0	352	US-10-617-217A-75	Sequence 75, App1
8	1831	100.0	352	US-10-024-298A-75	Sequence 75, App1
9	1826	99.7	392	US-09-764-86A-801	Sequence 801, App
10	1824	99.6	352	US-10-024-298A-73	Sequence 73, App1
11	1824	99.6	352	US-10-042-211A-73	Sequence 73, App1
12	1824	99.6	352	US-10-617-217A-73	Sequence 73, App1
13	1824	99.6	352	US-10-024-298A-73	Sequence 73, App1
14	901	49.2	174	US-09-764-86A-1262	Sequence 1262, App
15	854	46.6	165	US-10-264-237-2680	Sequence 2680, App
16	442.5	24.2	338	US-11-097-143-411	Sequence 411, App
17	295	16.1	339	US-10-424-599-158556	Sequence 158556, App
18	288.5	15.8	343	US-10-425-115-364826	Sequence 364826, App
19	267.5	14.6	338	US-10-739-930-6185	Sequence 6185, App
20	262	14.3	350	US-10-425-115-364805	Sequence 364805, App
21	252.5	13.8	375	US-10-739-930-10614	Sequence 10614, App
22	231	12.6	232	US-10-425-114-47706	Sequence 47706, App
23	214	11.7	358	US-10-424-599-224671	Sequence 224671, App
24	195.5	11.6	310	US-10-437-963-111394	Sequence 111394, App
25	193.5	10.7	378	US-10-437-963-111394	Sequence 111394, App
26	188.5	10.3	332	US-10-195-144-83	Sequence 83, App1
27	188.5	10.3	332	US-10-345-072-83	Sequence 83, App1

28	184.5	10.1	163	US-10-425-114-65305	Sequence 65305, App
29	183	10.0	236	US-10-425-114-38446	Sequence 38446, App
30	183	10.0	236	US-10-425-115-253264	Sequence 253264, App
31	172	9.4	366	US-10-739-930-7102	Sequence 7102, App
32	163	8.9	257	US-09-949-842-14	Sequence 14, App1
33	163	8.9	403	US-10-087-192-114	Sequence 114, App1
34	155.5	8.5	303	US-10-094-749-2475	Sequence 2475, App
35	155.5	8.5	696	US-10-094-749-2425	Sequence 2425, App
36	155.5	8.5	723	US-10-104-047-2572	Sequence 2572, App
37	151	8.2	700	US-11-097-143-25191	Sequence 25191, App
38	148.5	8.1	272	US-10-108-260A-4608	Sequence 4608, App
39	145.5	7.9	336	US-10-451-168-89	Sequence 89, App1
40	145.5	7.9	336	US-10-980-387-89	Sequence 89, App1
41	144.5	7.9	169	US-10-425-115-364837	Sequence 364837, App
42	144.5	7.9	438	US-08-464-588-2	Sequence 2, App1
43	144.5	7.9	438	US-10-323-643-2	Sequence 2, App1
44	144.5	7.9	618	US-10-153-668-338	Sequence 338, App
45	144.5	7.9	618	US-10-207-655-200	Sequence 200, App

ALIGNMENTS

RESULT 1

US-09-978-360A-437
Sequence 437, Application US/0978360A
Publication No. US20040110939A1
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste Dumas Malne
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
APPLICANT: Clusel, Catherine
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56, USA, CIP
CURRENT APPLICATION NUMBER: US/09/978, 360A
PRIORITY FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/066, 677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/069, 957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/074, 121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/081, 563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/096, 116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/099, 273
PRIOR FILING DATE: -09-04
PRIOR APPLICATION NUMBER: US 09/191, 997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215, 435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247, 155
PRIOR FILING DATE: 1999-02-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent.pm
SEQ ID NO 437
LENGTH: 352
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -23...-1
US-09-978-360A-437
Query Match 100.0%, Score 1831, DB 3, Length 352;
Best Local Similarity 100.0%, Pred. No. 1, 1e-162;
Matches 352, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

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QY 1 MESGRPSLCOFILIGTTSVYTAALYSYRQKARVSQELKGAKVHLGEDLKSILSEAPG 60
DB 1 MESGRPSLCOFILIGTTSVYTAALYSYRQKARVSQELKGAKVHLGEDLKSILSEAPG 60
QY 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIQRLTLOEHKVMWNRTHLMNDCSKI1HOR 120
DB 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIQRLTLOEHKVMWNRTHLMNDCSKI1HOR 120
QY 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180
DB 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180
QY 181 GIOETEMLKVGATLTGVELVLDDNSVRLQPPKQMOYLLSODPDSLQROESSVRLW 240
DB 181 GIOETEMLKVGATLTGVELVLDDNSVRLQPPKQMOYLLSODPDSLQROESSVRLW 240
QY 241 KVALVFGFATCATLFFILRKQYLOQROERLRLKQMOEFQEHBAQLLSRAKPEDRESLKS 300
DB 241 KVALVFGFATCATLFFILRKQYLOQROERLRLKQMOEFQEHBAQLLSRAKPEDRESLKS 300
QY 301 ACVVCLSFSCVFLGCGHVCSTECYRALPEPKKCPICROAITRVIPLVNS 352
DB 301 ACVVCLSFSCVFLGCGHVCSTECYRALPEPKKCPICROAITRVIPLVNS 352

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RESULT 2

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US-10-024-298A-75
/ Sequence 75, Application US/10024298A
/ Publication No. US20030143540A1
/ GENERAL INFORMATION:
/ APPLICANT: ASAMI KASEI KABUSHIKI KAISHA
/ APPLICANT: AKIO MATSUDA
/ APPLICANT: GOICHI HONDA
/ APPLICANT: SHUJI MURAMATSU
/ APPLICANT: YUKIKO NAGANO
/ TITLE OF INVENTION: NF-K B Activating Gene
/ FILE REFERENCE: 1254-0191P
/ CURRENT APPLICATION NUMBER: US/10/024,298A
/ PRIOR FILING DATE: 2003-04-08
/ PRIOR APPLICATION NUMBER: 60/314,385
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: 60/278,641
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: 60/258,315
/ PRIOR FILING DATE: 2000-12-28
/ PRIOR APPLICATION NUMBER: JP254018/2001
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: JP0088912/2001
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: JP402286/2000
/ PRIOR FILING DATE: 2000-12-28
/ NUMBER OF SEQ ID NOS: 182
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 75
/ LENGTH: 352
/ TYPE: PRN
/ ORGANISM: Homo sapiens
US-10-024-298A-75

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Query Match 100.0%; Score 1831; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1,1e-162;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESGRPSLCOFILIGTTSVYTAALYSYRQKARVSQELKGAKVHLGEDLKSILSEAPG 60
DB 1 MESGRPSLCOFILIGTTSVYTAALYSYRQKARVSQELKGAKVHLGEDLKSILSEAPG 60
QY 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIQRLTLOEHKVMWNRTHLMNDCSKI1HOR 120
DB 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIQRLTLOEHKVMWNRTHLMNDCSKI1HOR 120
QY 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180
DB 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180

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DB 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180
QY 181 GIOETEMLKVGATLTGVELVLDDNSVRLQPPKQMOYLLSODPDSLQROESSVRLW 240
DB 181 GIOETEMLKVGATLTGVELVLDDNSVRLQPPKQMOYLLSODPDSLQROESSVRLW 240
QY 241 KVALVFGFATCATLFFILRKQYLOQROERLRLKQMOEFQEHBAQLLSRAKPEDRESLKS 300
DB 241 KVALVFGFATCATLFFILRKQYLOQROERLRLKQMOEFQEHBAQLLSRAKPEDRESLKS 300
QY 301 ACVVCLSFSCVFLGCGHVCSTECYRALPEPKKCPICROAITRVIPLVNS 352
DB 301 ACVVCLSFSCVFLGCGHVCSTECYRALPEPKKCPICROAITRVIPLVNS 352

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RESULT 3

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US-10-042-211A-75
/ Sequence 75, Application US/10042211A
/ Publication No. US20030170719A1
/ GENERAL INFORMATION:
/ APPLICANT: MATSUDA, AKIO et al.
/ TITLE OF INVENTION: NFkB Activating Gene
/ FILE REFERENCE: 1254-0192P
/ CURRENT APPLICATION NUMBER: US/10/042,211A
/ PRIOR FILING DATE: 2002-01-11
/ PRIOR APPLICATION NUMBER: JP 2000-402288
/ PRIOR FILING DATE: 2000-12-28
/ PRIOR APPLICATION NUMBER: JP 2001-088912
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: JP 2001-254018
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: US 60/258,315
/ PRIOR FILING DATE: 2000-12-28
/ PRIOR APPLICATION NUMBER: US 60/278,640
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: US 60/314,385
/ PRIOR FILING DATE: 2001-08-24
/ NUMBER OF SEQ ID NOS: 182
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 75
/ LENGTH: 352
/ TYPE: PRN
/ ORGANISM: Homo sapiens
US-10-042-211A-75

```

```

Query Match 100.0%; Score 1831; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1,1e-162;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESGRPSLCOFILIGTTSVYTAALYSYRQKARVSQELKGAKVHLGEDLKSILSEAPG 60
DB 1 MESGRPSLCOFILIGTTSVYTAALYSYRQKARVSQELKGAKVHLGEDLKSILSEAPG 60
QY 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIQRLTLOEHKVMWNRTHLMNDCSKI1HOR 120
DB 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIQRLTLOEHKVMWNRTHLMNDCSKI1HOR 120
QY 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180
DB 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLFTVYEKFPHSIOSFTDVIIGHYISGERPK 180
QY 181 GIOETEMLKVGATLTGVELVLDDNSVRLQPPKQMOYLLSODPDSLQROESSVRLW 240
DB 181 GIOETEMLKVGATLTGVELVLDDNSVRLQPPKQMOYLLSODPDSLQROESSVRLW 240
QY 241 KVALVFGFATCATLFFILRKQYLOQROERLRLKQMOEFQEHBAQLLSRAKPEDRESLKS 300
DB 241 KVALVFGFATCATLFFILRKQYLOQROERLRLKQMOEFQEHBAQLLSRAKPEDRESLKS 300
QY 301 ACVVCLSFSCVFLGCGHVCSTECYRALPEPKKCPICROAITRVIPLVNS 352
DB 301 ACVVCLSFSCVFLGCGHVCSTECYRALPEPKKCPICROAITRVIPLVNS 352

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RESULT 4
US-10-315-664-105
; Sequence 105, Application US/10315664
; Publication No. US20030203377A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bouguetieret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal
; FILE REFERENCE: GENSET.050CP3
; CURRENT FILING DATE: US/10/315,664
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/599,360
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 105
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -23...-1
US-10-315-664-105

Query Match
Best Local Similarity 100.0%; Score 1831; DB 4; Length 352;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGRPSLCOPFILLGTTSVTTAALYSYVRKARVSQELKAKVHGLGEDIKSLISEAPG 60
DB 1 MESGRPSLCOPFILLGTTSVTTAALYSYVRKARVSQELKAKVHGLGEDIKSLISEAPG 60
QY 61 KCVPAVAVGAVRSYKETLNSQFVENCCKGVORLTLOEHKVMWNRTHLMDCKIIR 120
DB 61 KCVPAVAVGAVRSYKETLNSQFVENCCKGVORLTLOEHKVMWNRTHLMDCKIIR 120
QY 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLETYEKHPSIQSFVDVIGHYISGERPK 180
DB 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLETYEKHPSIQSFVDVIGHYISGERPK 180
QY 181 GIQTEEMLKVGATLTGVELVLDNNSVRLQPPKQGMYYLSSQDPDSLQROESSVRLM 240
DB 181 GIQTEEMLKVGATLTGVELVLDNNSVRLQPPKQGMYYLSSQDPDSLQROESSVRLM 240
QY 241 KVLAVFGFATCATLFFILRKQYLRQERLRLKQOEFOHEQQLSRAPEDRESLKS 300
DB 241 KVLAVFGFATCATLFFILRKQYLRQERLRLKQOEFOHEQQLSRAPEDRESLKS 300
QY 301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKCPICROAIRVPIPLNS 352
DB 301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKCPICROAIRVPIPLNS 352

RESULT 5
US-10-221-625-25
; Sequence 25, Application US/10221625
; Publication No. US20040033942A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HILMAN, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: LU, Dying Aina M.

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; APPLICANT: PATTERSON, Chandra
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BANDMAN, Olga
; APPLICANT: TANG, Y. Tom
; APPLICANT: MATHUR, Preeti
; APPLICANT: SHAH, Puri
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: REDDY, Roopa
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: PF-0761 PCT
; CURRENT FILING DATE: US/10/221,625
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PERL Program
; SEQ ID NO 25
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040033942A1 1383473CD1
US-10-221-625-25

Query Match
Best Local Similarity 100.0%; Score 1831; DB 4; Length 352;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGRPSLCOPFILLGTTSVTTAALYSYVRKARVSQELKAKVHGLGEDIKSLISEAPG 60
DB 1 MESGRPSLCOPFILLGTTSVTTAALYSYVRKARVSQELKAKVHGLGEDIKSLISEAPG 60
QY 61 KCVPAVAVGAVRSYKETLNSQFVENCCKGVORLTLOEHKVMWNRTHLMDCKIIR 120
DB 61 KCVPAVAVGAVRSYKETLNSQFVENCCKGVORLTLOEHKVMWNRTHLMDCKIIR 120
QY 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLETYEKHPSIQSFVDVIGHYISGERPK 180
DB 121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLETYEKHPSIQSFVDVIGHYISGERPK 180
QY 181 GIQTEEMLKVGATLTGVELVLDNNSVRLQPPKQGMYYLSSQDPDSLQROESSVRLM 240
DB 181 GIQTEEMLKVGATLTGVELVLDNNSVRLQPPKQGMYYLSSQDPDSLQROESSVRLM 240
QY 241 KVLAVFGFATCATLFFILRKQYLRQERLRLKQOEFOHEQQLSRAPEDRESLKS 300
DB 241 KVLAVFGFATCATLFFILRKQYLRQERLRLKQOEFOHEQQLSRAPEDRESLKS 300
QY 301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKCPICROAIRVPIPLNS 352
DB 301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKCPICROAIRVPIPLNS 352

RESULT 6
US-10-169-395-92
; Sequence 92, Application US/10169395
; Publication No. US20040034192A1
; GENERAL INFORMATION:
; APPLICANT: KATO, Seishi
; APPLICANT: KIMURA, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING
; FILE REFERENCE: 01997.015100.US
; CURRENT FILING DATE: US/10/169,395
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: JP 2000-585
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-588
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-2299
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-26862
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: JP 2000-58367

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; PRIOR FILING DATE: 2000-03-03
 ; PRIOR APPLICATION NUMBER: PCT/JP00/09359
 ; PRIOR FILING DATE: 2000-12-28
 ; NUMBER OF SEQ ID NOS: 150
 ; SEQ ID NO 92
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-169-395-92

Query Match 100.0%; Score 1831; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1,1e-162;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQARVSOELKGAKVHLGSDLSISEAPG 60
 DB 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQARVSOELKGAKVHLGSDLSISEAPG 60
 QY 61 KCPYAVIBGAVSVKETSINSQFVENCCKVIGRLTLOEHKVMNRTTHLMDCKIIHOR 120
 DB 61 KCPYAVIBGAVSVKETSINSQFVENCCKVIGRLTLOEHKVMNRTTHLMDCKIIHOR 120
 QY 121 TMTVPDLYPHEDGVAVRVLKPLDSVDLGLETYKFPSPISQFTDVIIGHYISGERPK 180
 DB 121 TMTVPDLYPHEDGVAVRVLKPLDSVDLGLETYKFPSPISQFTDVIIGHYISGERPK 180
 QY 181 GIOETEMLKVGATLTGVELVDNNSVRLQPKQMGYYLSQDFSLOROSSVRLW 240
 DB 181 GIOETEMLKVGATLTGVELVDNNSVRLQPKQMGYYLSQDFSLOROSSVRLW 240
 QY 241 KYLAVFGPATCATLFFILRKQYLRORRLKQOEFOHEAQLLSRAKPEDRESLKS 300
 DB 241 KYLAVFGPATCATLFFILRKQYLRORRLKQOEFOHEAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLISFKSCVFLGCHVCSCTECYRALPEPKKCPICROAIRVPIPLVNS 352
 DB 301 ACVCLISFKSCVFLGCHVCSCTECYRALPEPKKCPICROAIRVPIPLVNS 352

RESULT 7

US-10-617-217A-75
 ; Sequence 75, Application US/10617217A
 ; Publication No. US20040081986A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MATSUDA, Akio et al.
 ; TITLE OF INVENTION: NF-kB ACTIVATING GENE
 ; FILE REFERENCE: 1254-0229P
 ; CURRENT APPLICATION NUMBER: US/10/617, 217A
 ; PRIOR FILING DATE: 2003-07-11
 ; PRIOR APPLICATION NUMBER: JP 2000-402288
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: JP 2001-088912
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: JP 2001-254018
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/258,315
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: US 60/278,640
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: US 60/314,385
 ; PRIOR FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 75
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-617-217A-75

Query Match 100.0%; Score 1831; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1,1e-162;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQARVSOELKGAKVHLGSDLSISEAPG 60
 DB 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQARVSOELKGAKVHLGSDLSISEAPG 60
 QY 61 KCPYAVIBGAVSVKETSINSQFVENCCKVIGRLTLOEHKVMNRTTHLMDCKIIHOR 120
 DB 61 KCPYAVIBGAVSVKETSINSQFVENCCKVIGRLTLOEHKVMNRTTHLMDCKIIHOR 120
 QY 121 TMTVPDLYPHEDGVAVRVLKPLDSVDLGLETYKFPSPISQFTDVIIGHYISGERPK 180
 DB 121 TMTVPDLYPHEDGVAVRVLKPLDSVDLGLETYKFPSPISQFTDVIIGHYISGERPK 180
 QY 181 GIOETEMLKVGATLTGVELVDNNSVRLQPKQMGYYLSQDFSLOROSSVRLW 240
 DB 181 GIOETEMLKVGATLTGVELVDNNSVRLQPKQMGYYLSQDFSLOROSSVRLW 240
 QY 241 KYLAVFGPATCATLFFILRKQYLRORRLKQOEFOHEAQLLSRAKPEDRESLKS 300
 DB 241 KYLAVFGPATCATLFFILRKQYLRORRLKQOEFOHEAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLISFKSCVFLGCHVCSCTECYRALPEPKKCPICROAIRVPIPLVNS 352
 DB 301 ACVCLISFKSCVFLGCHVCSCTECYRALPEPKKCPICROAIRVPIPLVNS 352

RESULT 8

US-10-024-298A-75
 ; Sequence 75, Application US/10024298A
 ; Publication No. US20040214167A9
 ; GENERAL INFORMATION:
 ; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
 ; APPLICANT: AKIO MATSUDA
 ; APPLICANT: Goichi HONDA
 ; APPLICANT: Shuji MURAMATSU
 ; APPLICANT: Yukiko NAGANO
 ; TITLE OF INVENTION: NF-kB Activating Gene
 ; FILE REFERENCE: 1254-0191P
 ; CURRENT APPLICATION NUMBER: US/10/024, 298A
 ; PRIOR FILING DATE: 2003-04-08
 ; PRIOR APPLICATION NUMBER: 60/314,385
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: 60/278,641
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 60/258,315
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: JP254018/2001
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: JP0088912/2001
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: JP402288/2000
 ; PRIOR FILING DATE: 2000-12-28
 ; NUMBER OF SEQ ID NOS: 182
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 75
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-024-298A-75

Query Match 100.0%; Score 1831; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1,1e-162;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQARVSOELKGAKVHLGSDLSISEAPG 60
 DB 1 MESGGRPSLCQFILLGTTSVVTAALYSVYRQARVSOELKGAKVHLGSDLSISEAPG 60
 QY 61 KCPYAVIBGAVSVKETSINSQFVENCCKVIGRLTLOEHKVMNRTTHLMDCKIIHOR 120
 DB 61 KCPYAVIBGAVSVKETSINSQFVENCCKVIGRLTLOEHKVMNRTTHLMDCKIIHOR 120
 QY 121 TMTVPDLYPHEDGVAVRVLKPLDSVDLGLETYKFPSPISQFTDVIIGHYISGERPK 180
 DB 121 TMTVPDLYPHEDGVAVRVLKPLDSVDLGLETYKFPSPISQFTDVIIGHYISGERPK 180

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Db      121 TTTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLETYEKFPHSIQSFDTVIGHYISGERPK 180
Qy      181 G|O|E|E|M|K|G|A|T|T|G|V|E|L|D|N|N|S|V|R|L|O|P|K|G|M|Q|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 240
        181 G|O|E|E|M|K|G|A|T|T|G|V|E|L|D|N|N|S|V|R|L|O|P|K|G|M|Q|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 240
Qy      241 K|V|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|E|R|L|R|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
        241 K|V|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|E|R|L|R|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
Db      241 K|V|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|E|R|L|R|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
Qy      301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|S|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352
        301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|S|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352
Db      301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|S|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352

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RESULT 9
US-09-764-864-801
Sequence 801, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 801
LENGTH: 392
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE: NAME/KEY: SITE
LOCATION: (238)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-801

Query Match 99.7%; Score 1826; DB 3; Length 392;
Best Local Similarity 99.7%; Pred. No. 3.7e-162;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 M|E|S|G|R|P|S|L|C|O|F|I|L|G|T|S|V|T|A|L|Y|S|V|R|Q|R|A|R|V|S|O|E|L|K|G|K|V|H|L|G|E|D|L|S|I|S|E|A|R|G| 60
        41 M|E|S|G|R|P|S|L|C|O|F|I|L|G|T|S|V|T|A|L|Y|S|V|R|Q|R|A|R|V|S|O|E|L|K|G|K|V|H|L|G|E|D|L|S|I|S|E|A|R|G| 100
Db      41 M|E|S|G|R|P|S|L|C|O|F|I|L|G|T|S|V|T|A|L|Y|S|V|R|Q|R|A|R|V|S|O|E|L|K|G|K|V|H|L|G|E|D|L|S|I|S|E|A|R|G| 100
Qy      61 K|C|V|P|A|V|E|G|A|R|S|V|E|T|I|N|S|Q|F|E|N|C|K|G|V|I|O|R|L|T|O|E|H|K|W|N|R|T|H|L|M|N|D|S|K|I|H|O|R| 120
        101 K|C|V|P|A|V|E|G|A|R|S|V|E|T|I|N|S|Q|F|E|N|C|K|G|V|I|O|R|L|T|O|E|H|K|W|N|R|T|H|L|M|N|D|S|K|I|H|O|R| 160
Db      101 K|C|V|P|A|V|E|G|A|R|S|V|E|T|I|N|S|Q|F|E|N|C|K|G|V|I|O|R|L|T|O|E|H|K|W|N|R|T|H|L|M|N|D|S|K|I|H|O|R| 160
Qy      121 T|N|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|V|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|F|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 180
        121 T|N|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|V|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|F|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 180
Db      121 T|N|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|V|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|F|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 180
Qy      161 T|T|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|V|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|F|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 220
        161 T|T|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|V|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|F|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 220
Db      161 T|T|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|V|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|F|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 220
Qy      181 G|I|O|E|E|M|K|G|A|T|T|G|V|E|L|D|N|N|S|V|R|L|O|P|K|G|M|Q|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 240
        181 G|I|O|E|E|M|K|G|A|T|T|G|V|E|L|D|N|N|S|V|R|L|O|P|K|G|M|Q|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 240
Db      221 G|I|O|E|E|M|K|G|A|T|T|G|V|E|L|D|N|N|S|V|R|L|O|P|K|G|M|Q|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 280
        221 G|I|O|E|E|M|K|G|A|T|T|G|V|E|L|D|N|N|S|V|R|L|O|P|K|G|M|Q|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 280
Qy      241 K|V|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|E|R|L|R|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
        241 K|V|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|E|R|L|R|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
Db      281 K|V|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|E|R|L|R|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 340
        281 K|V|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|E|R|L|R|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 340
Qy      301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|S|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352
        301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|S|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352
Db      341 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|S|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 392
        341 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|S|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 392

```

RESULT 10
US-10-024-298A-73
Sequence 73, Application US/10024298A
Publication No. US20030143540A1
GENERAL INFORMATION:
APPLICANT: ASAMI KASEI KABUSHIKI KAISHA

```

; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 73
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-73
Query Match 99.6%; Score 1824; DB 4; Length 352;
Best Local Similarity 99.7%; Pred. No. 4.9e-162;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 M|E|S|G|R|P|S|L|C|O|F|I|L|G|T|S|V|T|A|L|Y|S|V|R|Q|R|A|R|V|S|O|E|L|K|G|K|V|H|L|G|E|D|L|S|I|S|E|A|R|G| 60
        1 M|E|S|G|R|P|S|L|C|O|F|I|L|G|T|S|V|T|A|L|Y|S|V|R|Q|R|A|R|V|S|O|E|L|K|G|K|V|H|L|G|E|D|L|S|I|S|E|A|R|G| 60
Db      1 M|E|S|G|R|P|S|L|C|O|F|I|L|G|T|S|V|T|A|L|Y|S|V|R|Q|R|A|R|V|S|O|E|L|K|G|K|V|H|L|G|E|D|L|S|I|S|E|A|R|G| 60
Qy      61 K|C|V|P|A|V|E|G|A|R|S|V|E|T|I|N|S|Q|F|E|N|C|K|G|V|I|O|R|L|T|O|E|H|K|W|N|R|T|H|L|M|N|D|S|K|I|H|O|R| 120
        61 K|C|V|P|A|V|E|G|A|R|S|V|E|T|I|N|S|Q|F|E|N|C|K|G|V|I|O|R|L|T|O|E|H|K|W|N|R|T|H|L|M|N|D|S|K|I|H|O|R| 120
Db      61 K|C|V|P|A|V|E|G|A|R|S|V|E|T|I|N|S|Q|F|E|N|C|K|G|V|I|O|R|L|T|O|E|H|K|W|N|R|T|H|L|M|N|D|S|K|I|H|O|R| 120
Qy      121 T|N|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|V|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|F|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 180
        121 T|N|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|V|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|F|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 180
Db      121 T|N|T|V|P|D|L|V|P|H|E|D|G|V|D|A|V|R|V|L|K|P|L|D|S|V|D|L|G|E|T|Y|E|K|F|H|P|S|I|Q|S|F|T|D|V|I|G|H|Y|I|S|G|E|R|P|K| 180
Qy      161 G|I|O|E|E|M|K|G|A|T|T|G|V|E|L|D|N|N|S|V|R|L|O|P|K|G|M|Q|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 240
        161 G|I|O|E|E|M|K|G|A|T|T|G|V|E|L|D|N|N|S|V|R|L|O|P|K|G|M|Q|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 240
Db      161 G|I|O|E|E|M|K|G|A|T|T|G|V|E|L|D|N|N|S|V|R|L|O|P|K|G|M|Q|Y|L|S|S|O|P|D|S|L|O|Q|E|S|V|R|L| 240
Qy      241 K|V|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|E|R|L|R|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
        241 K|V|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|E|R|L|R|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
Db      241 K|V|A|V|F|G|P|A|T|C|A|T|F|I|L|R|K|O|Y|L|O|R|E|R|L|R|K|O|Q|E|F|O|E|H|A|O|L|S|R|A|K|P|E|D|R|E|S|L|K|S| 300
Qy      301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|S|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352
        301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|S|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352
Db      301 A|C|V|C|L|S|F|K|S|C|V|F|E|C|G|H|V|C|S|T|E|C|Y|R|A|L|P|E|P|K|C|P|I|C|R|O|A|I|T|R|V|I|P|L|Y|N|S| 352

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RESULT 11
US-10-042-211A-73
Sequence 73, Application US/10042211A
Publication No. US20030170719A1
GENERAL INFORMATION:
APPLICANT: MATSUDA, AKIO et al.
TITLE OF INVENTION: NFkB Activating Gene
FILE REFERENCE: 1254-0192P
CURRENT APPLICATION NUMBER: US/10/042,211A
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: JP 2000-402288
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP 2001-088912
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 2001-254018
PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/258,315
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: US 60/278,640
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: US 60/314,385
 ; PRIOR FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 182
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 73
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-042-211A-73

Query Match 99.6%; Score 1824; DB 4; Length 352;
 Best Local Similarity 99.7%; Pred. No. 4.9e-162;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESSGRPSLCOFILGTTSVTTAALYSVYRQKARVSOELKGAKKVLHGEDLKSILSEAPG 60
 DB 1 MESSGRPSLCOFILGTTSVTTAALYSVYRQKARVSOELKGAKKVLHGEDLKSILSEAPG 60
 QY 61 KCVPAVIEGAVRSYKETLNSQFVENCKVYORLTLOEHKVMNRTTHLMNDCSKIIHOR 120
 DB 61 KCVPAVIEGAVRSYKETLNSQFVENCKVYORLTLOEHKVMNRTTHLMNDCSKIIHOR 120
 QY 121 TMTVPDLVPHEDGVDAVAVLKPDLSDVLDGLEYEKFPHSIOSFTVIGHYISGERPK 180
 DB 121 TMTVPDLVPHEDGVDAVAVLKPDLSDVLDGLEYEKFPHSIOSFTVIGHYISGERPK 180
 QY 181 GIOETEMLVKVGATLTGVELVLDNNSVRLQPKQMGVYLSQDPDSLQROESSVRLM 240
 DB 181 GIOETEMLVKVGATLTGVELVLDNNSVRLQPKQMGVYLSQDPDSLQROESSVRLM 240
 QY 241 KVLAVFGPATCATLFFILRKQYLOROERLRLKOMQEFQEHQAQLLSRAKPEDRESLKS 300
 DB 241 KVLAVFGPATCATLFFILRKQYLOROERLRLKOMQEFQEHQAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSPKSCVFLKCGHVCSTCECYRALPEPKKPCICROAITRVIPYNS 352
 DB 301 ACVCLSSPKSCVFLKCGHVCSTCECYRALPEPKKPCICROAITRVIPYNS 352

RESULT 12
 US-10-617-217A-73
 ; Sequence 73, Application US/10617217A
 ; Publication No. US20040081986A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MATSUDA, Akio et al.
 ; TITLE OF INVENTION: NF-kB ACTIVATING GENE
 ; FILE REFERENCE: 1254-0229P
 ; CURRENT APPLICATION NUMBER: US/10/617,217A
 ; PRIOR FILING DATE: 2003-07-11
 ; PRIOR APPLICATION NUMBER: JP 2000-402288
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: JP 2001-088912
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: JP 2001-254018
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/258,315
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: US 60/278,640
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: US 60/314,385
 ; PRIOR FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 73
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-617-217A-73

Query Match 99.6%; Score 1824; DB 4; Length 352;
 Best Local Similarity 99.7%; Pred. No. 4.9e-162;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESSGRPSLCOFILGTTSVTTAALYSVYRQKARVSOELKGAKKVLHGEDLKSILSEAPG 60
 DB 1 MESSGRPSLCOFILGTTSVTTAALYSVYRQKARVSOELKGAKKVLHGEDLKSILSEAPG 60
 QY 61 KCVPAVIEGAVRSYKETLNSQFVENCKVYORLTLOEHKVMNRTTHLMNDCSKIIHOR 120
 DB 61 KCVPAVIEGAVRSYKETLNSQFVENCKVYORLTLOEHKVMNRTTHLMNDCSKIIHOR 120
 QY 121 TMTVPDLVPHEDGVDAVAVLKPDLSDVLDGLEYEKFPHSIOSFTVIGHYISGERPK 180
 DB 121 TMTVPDLVPHEDGVDAVAVLKPDLSDVLDGLEYEKFPHSIOSFTVIGHYISGERPK 180
 QY 181 GIOETEMLVKVGATLTGVELVLDNNSVRLQPKQMGVYLSQDPDSLQROESSVRLM 240
 DB 181 GIOETEMLVKVGATLTGVELVLDNNSVRLQPKQMGVYLSQDPDSLQROESSVRLM 240
 QY 241 KVLAVFGPATCATLFFILRKQYLOROERLRLKOMQEFQEHQAQLLSRAKPEDRESLKS 300
 DB 241 KVLAVFGPATCATLFFILRKQYLOROERLRLKOMQEFQEHQAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSPKSCVFLKCGHVCSTCECYRALPEPKKPCICROAITRVIPYNS 352
 DB 301 ACVCLSSPKSCVFLKCGHVCSTCECYRALPEPKKPCICROAITRVIPYNS 352

RESULT 13
 US-10-024-298A-73
 ; Sequence 73, Application US/10024298A
 ; Publication No. US20040214167A9
 ; GENERAL INFORMATION:
 ; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
 ; APPLICANT: AKIO MATSUDA
 ; APPLICANT: GOICHI HONDA
 ; APPLICANT: SHUKI MURAMATSU
 ; APPLICANT: YUKIKO NAGANO
 ; TITLE OF INVENTION: NF-kB Activating Gene
 ; FILE REFERENCE: 1254-0191P
 ; CURRENT APPLICATION NUMBER: US/10/024,298A
 ; PRIOR FILING DATE: 2003-04-08
 ; PRIOR APPLICATION NUMBER: 60/314,385
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: 60/278,641
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 60/258,315
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: JP254018/2001
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: JP0088912/2001
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: JP402288/2000
 ; PRIOR FILING DATE: 2000-12-28
 ; NUMBER OF SEQ ID NOS: 182
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 73
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-024-298A-73

Query Match 99.6%; Score 1824; DB 4; Length 352;
 Best Local Similarity 99.7%; Pred. No. 4.9e-162;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESSGRPSLCOFILGTTSVTTAALYSVYRQKARVSOELKGAKKVLHGEDLKSILSEAPG 60
 DB 1 MESSGRPSLCOFILGTTSVTTAALYSVYRQKARVSOELKGAKKVLHGEDLKSILSEAPG 60
 QY 61 KCVPAVIEGAVRSYKETLNSQFVENCKVYORLTLOEHKVMNRTTHLMNDCSKIIHOR 120

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Db      61 KCPVAVIEGAVRSVETLNSQFVENCKVIOQLTQEHKVMWNRTHLMNDCSKIIHOR 120
QY      121 TMTVPDLVPHEDGDVAVRVLKPLDSVDLGHETVYEKHPISOSTVDYIGYISGERK 180
Db      121 TMTVPDLVPHEDGDVAVRVLKPLDSVDLGHETVYEKHPISOSTVDYIGYISGERK 180
QY      181 GIOFTEEMLKVGATLTGVELVDNNSVRLQPPKQGMQYLLSSODPDSLQROESSVRLM 240
Db      181 GIOFTEEMLKVGATLTGVELVDNNSVRLQPPKQGMQYLLSSODPDSLQROESSVRLM 240
QY      241 KVLALVFGFATCATLFFILRKQYLOEROERLRLKQMOEFQEHQAQLLSRAKPEDRESLSK 300
Db      241 KVLALVFGFATCATLFFILRKQYLOEROERLRLKQMOEFQEHQAQLLSRAKPEDRESLSK 300
QY      301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKCPICROAITRVIPLYN 352
Db      301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKCPICROAITRVIPLYN 352

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RESULT 14

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US-09-764-864-1262
; Sequence 1262, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1262
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1262

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Query Match          49.2%; Score 901; DB 3; Length 174;
Best Local Similarity 99.4%; Pred. No. 6e-76; Indels 0; Gaps 0;
Matches 173; Conservative 0; Mismatches 1;

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QY      179 PKGIOETBEMLKVGATLTGVELVDNNSVRLQPPKQGMQYLLSSODPDSLQROESSVR 238
Db      1 PKGIOETBEMLKVGATLTGVELVDNNSVRLQPPKQGMQYLLSSODPDSLQROESSVR 60
QY      239 LMKVTLALVFGFATCATLFFILRKQYLOEROERLRLKQMOEFQEHQAQLLSRAKPEDRESL 298
Db      61 LMKVTLALVFGFATCATLFFILRKQYLOEROERLRLKQMOEFQEHQAQLLSRAKPEDRESL 120
QY      299 KSACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKCPICROAITRVIPLYN 352
Db      121 KSACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKCPICROAITRVIPLYN 174

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RESULT 15

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US-10-264-237-2680
; Sequence 2680, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2000-05-19

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; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2680
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (108)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2680

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Query Match          46.6%; Score 854; DB 4; Length 165;
Best Local Similarity 99.4%; Pred. No. 1.4e-71;
Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      188 MLKVGATLTGVELVDNNSVRLQPPKQGMQYLLSSODPDSLQROESSVRLMKVTLALVF 247
Db      1 MLKVGATLTGVELVDNNSVRLQPPKQGMQYLLSSODPDSLQROESSVRLMKVTLALVF 60
QY      248 GFATCATLFFILRKQYLOEROERLRLKQMOEFQEHQAQLLSRAKPEDRESLSKACVCL 307
Db      61 GFATCATLFFILRKQYLOEROERLRLKQMOEFQEHQAQLLSRAKPEDRESLSKACVCL 120
QY      308 SFKSCVFLFCGHVCSCTECYRALPEPKKCPICROAITRVIPLYN 352
Db      121 SFKSCVFLFCGHVCSCTECYRALPEPKKCPICROAITRVIPLYN 165

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Search completed: February 24, 2006, 08:57:45
Job time : 165 secs

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Db 241 KVALVGPATCATLFFILRKQYDQROERLRKQMOEFDEHRAQLSRAPKEDRSIKS 300

QY 301 ACVCSSFSKCVLECGHVCSTECYRALPEPKCPCIOATRVIPLYNS 352
Db 301 ACVCSSFSKCVLECGHVCSTECYRALPEPKCPCIOATRVIPLYNS 352

RESULT 2

US-08-905-223-421
Sequence 421, Application US/08905223
Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duclert, Americ
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 421:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
FEATURE:
NAME/KEY: sig_peptide
LOCATION: -23...-1
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 4.4
OTHER INFORMATION: seq 0FTILGTSVVA/AL
US-08-905-223-421

Query Match 24.3%; Score 445; DB 2; Length 91;

Best Local Similarity 98.9%; Pred. No. 5.8e-41;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESGGSPSLCQFTILGTSVVAALYSVYRKARVSOELKGAKVHLGDLKSLSEAG 60
Db 1 MESGGSPSLCQFTILGTSVVAALYSVYRKARVSOELKGAKVHLGDLKSLSEAG 60

QY 61 KCPYAVITGAVSVVETLNSQVENCXGY 90
Db 61 KCPYAVITGAVSVVETLNSQVENCXGY 90

RESULT 3
US-09-324-455-2

; Sequence 2, Application US/09324455
; Patent No. 6326481

; GENERAL INFORMATION:
; APPLICANT: yowe, David
; TITLE OF INVENTION: NOVEL MOLECULES OF THE AIP-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street
; CITY: Boston

; STATE: MA
; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/324,455

; FILING DATE: 02-JUN-1999
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/087,761

; FILING DATE: 02-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Weikie, John, Ph.D., Anita L.

; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/069001

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-324-455-2

Query Match 8.9%; Score 163; DB 2; Length 372;

Best Local Similarity 30.1%; Pred. No. 6.2e-09;
Matches 40; Conservative 29; Mismatches 48; Indels 16; Gaps 5;

QY 222 SQDPSDLSQROESSVR-LMRYLALVF-GRATCATLFFILRKQYDQROERLRKQMOEF 279
Db 254 SLSDLSIDVYEGMSVRQLKEILARNFVYSGCEKMEIYER-----VNRLYKEN 303

QY 280 OEHAQQLSRAPKEDRESLKSACVVCSSFSKCVLECGHVCSTECYRALPEPKCPCIC 339
Db 304 EBNQSYGERLQDDEP-DLICRICMDAYIDCVLLECGHVTCTKCGKRWSE---CPIIC 359

QY 340 RQATRVIPLYNS 352
Db 360 RQYVRAVHVFES 372

RESULT 4

US-09-434-408-2
Sequence 2, Application US/09434408

Patent No. 6440697

GENERAL INFORMATION:
APPLICANT: Grossmann, Angelika

APPLICANT: Venezia, Domenick
TITLE OF INVENTION: RING FINGER PROTEIN ZAPOR3

FILE REFERENCE: 98-41
CURRENT APPLICATION NUMBER: US/09/434,408

CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: US 60/108,258

EARLIER FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2
LENGTH: 723
TYPE: PRT
ORGANISM: Homo sapiens
US-09-434-408-2

Query Match 8.5%; Score 155.5; DB 2; Length 723;
Best Local Similarity 34.3%; Pred. No. 1.2e-07;
Matches 37; Conservative 16; Mismatches 36; Indels 17; Gaps 3;

QY 259 LKQYLRQERLRLKQMOEF-----QEHRALSLRAKPEDRESLSKACV 304
DB 618 LQHEILRRVQELLDARIQPELKPMPGEVVTPTAPQEPESVRPSAPPALELVQASECV 677
QY 305 CLASSFKCVPLECGHVCSTECYRALPEPKKCPICROAIVPIPLVNS 352
DB 678 CLERBAQMIPLNGHVCVCCQCCQCP-----RTCPICRODIAORLIYHS 722

RESULT 5
US-10-104-047-2572
Sequence 2572; Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2572
LENGTH: 723
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-2572

Query Match 8.5%; Score 155.5; DB 2; Length 723;
Best Local Similarity 34.3%; Pred. No. 1.2e-07;
Matches 37; Conservative 16; Mismatches 36; Indels 17; Gaps 3;

QY 259 LKQYLRQERLRLKQMOEF-----QEHRALSLRAKPEDRESLSKACV 304
DB 618 LQHEILRRVQELLDARIQPELKPMPGEVVTPTAPQEPESVRPSAPPALELVQASECV 677
QY 305 CLASSFKCVPLECGHVCSTECYRALPEPKKCPICROAIVPIPLVNS 352
DB 678 CLERBAQMIPLNGHVCVCCQCCQCP-----RTCPICRODIAORLIYHS 722

RESULT 6
US-09-270-767-58582
Sequence 58582; Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 58582
LENGTH: 350
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-58582

Query Match 8.2%; Score 151; DB 2; Length 350;

Best Local Similarity 31.5%; Pred. No. 1.2e-07;
Matches 34; Conservative 18; Mismatches 34; Indels 22; Gaps 3;

QY 264 LQROERLRLKQMOEFQEH-----EAQLLSRAK-----PEDRESLSKACV 304
DB 102 LKDEGLTVKQKJLVLMHRYDYKGCCEKQELDRVSLMTKMECPAVEKLADDELCKI 161
QY 305 CLASSFKCVPLECGHVCSTECYRALPEPKKCPICROAIVPIPLVNS 352
DB 162 CMDAPIECVPLECGHVMATCTSCGVKLVN---CPICROYIVAVVFFRA 206

RESULT 7
US-09-270-767-43239
Sequence 43239; Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 43239
LENGTH: 559
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43239

Query Match 8.2%; Score 151; DB 2; Length 559;
Best Local Similarity 31.5%; Pred. No. 2.5e-07;
Matches 34; Conservative 18; Mismatches 34; Indels 22; Gaps 3;

QY 264 LQROERLRLKQMOEFQEH-----EAQLLSRAK-----PEDRESLSKACV 304
DB 311 LKDEGLTVKQKJLVLMHRYDYKGCCEKQELDRVSLMTKMECPAVEKLADDELCKI 370
QY 305 CLASSFKCVPLECGHVCSTECYRALPEPKKCPICROAIVPIPLVNS 352
DB 371 CMDAPIECVPLECGHVMATCTSCGVKLVN---CPICROYIVAVVFFRA 415

RESULT 8
PCT-US95-05922A-2
Sequence 2; Application PC/TUS9505922A
GENERAL INFORMATION:
APPLICANT: HE, ET. AL.
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05922A
FILING DATE: 11 MAY 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

```

1 NAME: FERRARO, GREGORY D.
2 REGISTRATION NUMBER: 36,134
3 REFERENCE/DOCKET NUMBER: 325800-292
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 201-994-1700
6 TELEFAX: 201-994-1744
7 INFORMATION FOR SEQ ID NO: 2:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 438 AMINO ACIDS
10 TYPE: AMINO ACID
11 STRANDEDNESS:
12 TOPOLOGY: LINEAR
13 MOLECULE TYPE: PROTEIN
14 PCT-US95-05922A-2

```

[illegible]

RESULT 9
US-08-569-749-2
Sequence 2, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
TITLE OF INVENTION: David V
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarrasero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB

```

? TELECOMMUNICATION INFORMATION
? TELEPHONE: (415) 781-1989
? TELEFAX: (415) 398-3249
? INFORMATION FOR SEQ ID NO. 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 618 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULAR TYPE: protein
US-08-569-749-2

```

[illegible]

```

RESULT 10
US-09-069-023-29
; Sequence 29 Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069, 023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ. ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 618
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-069-023-29

```

Query Match	7.9%	Score 144.5;	DB 2;	Length 618;
Best Local Similarity	21.9%	Pred. No. 1.5e-06;		
Matches	68;	Conservative	50;	Mismatches 118; Indels 75; Gaps 13

QY	82	QV	E	N	K	E	K	V	I	O	R	L	T	L	O	E	H	K	W	M	N	R	T	L	M	D	S	C	K	I	H	O	R	N	T	P	F	L	V	H	E	D	G	V	A	N	V		141				
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
Db	343	E	F	V	D	L	O	G	R	P	H	L	-	E	Q	L	S	T	S	T	T	E	E	N	A	D	P	P	I	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
QY	142	L	K	P	L	-	D	S	V	D	L	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
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Db	392	N	T	P	V	K	S	A	L	E	M	G	F	N	R	D	I	V	K	O	T	S	K	I	L	T	T	O	E	N	K	T	N	D	I	V	S	A	L	L	N	A	D	E	K	E	E	K	O	A	E		451

QY 187 EMLKXGATLTGVGEL-----VLND-----NSVRLQPP---KQGMYYLSSOD--FD 227
DB 452 EMASDLSLIRKNRRAALFQQLTVCVLPILDNLLKANVINKQEHDIHKQTOPLQARLELD 511
QY 228 SLROESSVRLMKYALVFGFATCATLFFILRKOYLOQOE-----RLRLKQOEFOE 281
DB 512 TLVGNNAANIFKNCLEIDSTLYKNLFVDKMKYIPTEDVSGLSLEQJRLQOE--- 568
QY 282 HEAQLLSRAKPBDRSLKACVVCISSEKSCVPLECGHVCSTCEYRALPEPKCPICRQ 341
DB 569 -----RTCKVCMDKEVSVVFIPCGHLVVCQEC---APSLRKCPICRG 607
QY 342 AITRVIPLYNS 352
DB 608 IIKGTVRTFLS 618

RESULT 11

US-09-689-366-2
Sequence 2, Application US/09689366
Patent No. 6821736
GENERAL INFORMATION:
APPLICANT: Roche, Mike
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/689,366
FILING DATE: 10-Dec-2000
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE: 08-Dec-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-689-366-2

Query Match 7.9%; Score 144.5; DB 2; Length 618;
Best Local Similarity 21.9%; Pred. No. 1.5e-06;
Matches 68; Conservative 50; Mismatches 118; Indels 75; Gaps 13;
QY 82 QVFNCKGVYQRLTLOEHKMWNRTHLMNDCKSIHQRTNVPFDPVPHEDGVAVYAV 141
DB 343 EFDVDEIQGRYPHL--EQLLSTSDTGTGENADPPIIH-----FGGSSSSSDAVMM 391
QY 142 LKPL--DSVDLGL-----ETVYEKFPHSIQSF---TDVIGHYISGERPKGIOE---TE 186

DB 392 NTPVKSALENGPNRDLVKQTVOSKILTTGNNYKTVDIVSALINADEKRESEKQAE 451
QY 187 EMLKXGATLTGVGEL-----VLND-----NSVRLQPP---KQGMYYLSSOD--FD 227
DB 452 EMASDLSLIRKNRRAALFQQLTVCVLPILDNLLKANVINKQEHDIHKQTOPLQARLELD 511
QY 228 SLROESSVRLMKYALVFGFATCATLFFILRKOYLOQOE-----RLRLKQOEFOE 281
DB 512 TLVGNNAANIFKNCLEIDSTLYKNLFVDKMKYIPTEDVSGLSLEQJRLQOE--- 568
QY 282 HEAQLLSRAKPBDRSLKACVVCISSEKSCVPLECGHVCSTCEYRALPEPKCPICRQ 341
DB 569 -----RTCKVCMDKEVSVVFIPCGHLVVCQEC---APSLRKCPICRG 607
QY 342 AITRVIPLYNS 352
DB 608 IIKGTVRTFLS 618

RESULT 12

US-10-232-286-2
Sequence 2, Application US/10232286
Patent No. 6855815
GENERAL INFORMATION:
APPLICANT: Roche, Mike
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,286
FILING DATE: 30-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-232-286-2

Query Match 7.9%; Score 144.5; DB 2; Length 618;
Best Local Similarity 21.9%; Pred. No. 1.5e-06;
Matches 68; Conservative 50; Mismatches 118; Indels 75; Gaps 13;
QY 82 QVFNCKGVYQRLTLOEHKMWNRTHLMNDCKSIHQRTNVPFDPVPHEDGVAVYAV 141
DB 343 EFDVDEIQGRYPHL--EQLLSTSDTGTGENADPPIIH-----FGGSSSSSDAVMM 391
QY 142 LKPL--DSVDLGL-----ETVYEKFPHSIQSF---TDVIGHYISGERPKGIOE---TE 186

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Db      392 NTFVVKASLEMGFNRDLVKQTQVSKITLTGENTVTVDIVSALINAEDEKREBEKEKQAE
Qy      187 EMLKVGATLTGVEL-----VLDN---NSVRLQPP---KQGMQYLLSSQD-FD 227
Db      452 EMASDDLSTLRKNMAALFQQLTCVLPILDNLKANVINKQEHDIIRKQKQIPLOARELID 511
Qy      228 SLQROESSVRLMKVLALVFGATCATLFFILRKQYLOQOE-----RLRKQMOEERFOE 281
Db      512 TLIVKGNMAANIFKQCLKEIDSTLYKNLFVDKNMKYIPIEDVSGLSLEQRLRLOEE--- 568
Qy      282 HEAQLSRAKPEDRESLSKACVCLSSPKSCVFLGCHVCSCTEGYRALPEPKKPCICRQ 341
Db      569 -----RTCKVCMDEKESVVFICGHLVYQEC---APSLRKPICRG 607
Qy      342 AITRVIPLYNS 352
Db      608 IIKGTVRTPLS 618

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RESULT 13
PCT-US96-12860-2
; Sequence 2, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-12860-2

```

```

Query Match      7.8%; Score 144.5; DB 4; Length 618;
Best Local Similarity 21.9%; Pred. No. 1.5e-06;
Matches 68; Conservative 50; Mismatches 118; Indels 75; Gaps 13;
Qy      82 OFVENCKGYQRTLTQEHKVMNRTTHLWNSDKIIRHRTNTVPRDLVHEGCVDAARV 141
Db      343 ERFDEIGQKYPHL--EQILISTDTTGEENADPPH-----FGGESSSDDAVMM 391
Qy      142 LKPL--DSVDLGI-----ETVVEKFPISIQF--TDVIGHYISGERKQIOE---TE 186
Db      392 NTFVVKASLEMGFNRDLVKQTQVSKITLTGENTVTVDIVSALINAEDEKREBEKEKQAE 451

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Qy      187 EMLKVGATLTGVEL-----VLDN---NSVRLQPP---KQGMQYLLSSQD-FD 227
Db      452 EMASDDLSTLRKNMAALFQQLTCVLPILDNLKANVINKQEHDIIRKQKQIPLOARELID 511
Qy      228 SLQROESSVRLMKVLALVFGATCATLFFILRKQYLOQOE-----RLRKQMOEERFOE 281
Db      512 TLIVKGNMAANIFKQCLKEIDSTLYKNLFVDKNMKYIPIEDVSGLSLEQRLRLOEE--- 568
Qy      282 HEAQLSRAKPEDRESLSKACVCLSSPKSCVFLGCHVCSCTEGYRALPEPKKPCICRQ 341
Db      569 -----RTCKVCMDEKESVVFICGHLVYQEC---APSLRKPICRG 607
Qy      342 AITRVIPLYNS 352
Db      608 IIKGTVRTPLS 618

```

```

RESULT 14
US-10-104-047-3425
; Sequence 3425, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3425
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3425

```

```

Query Match      7.8%; Score 143.5; DB 2; Length 363;
Best Local Similarity 30.1%; Pred. No. 8.3e-07;
Matches 41; Conservative 28; Mismatches 40; Indels 27; Gaps 7;
Qy      224 QDFDSLQROESSVRLMKVLALVFGATCATLFFILRKQYLOQOEERLRLKQMOEERFOE 281
Db      248 EDIBGLTVRQ-----LKEILARNPVNYKGCCEKEKELM-----ERVTRLYKQKGLQ- 293
Qy      282 HEAQLSRAKPEDRESLSKACVCLSSPKSCVFLGCHVCSCTEGYRALPEPKKPC 336
Db      294 --HIVSGABDONGGAVSGGLEENLCKICMDSPIDCVLLEGHVTCTKCGKRMNE---C 347
Qy      337 PICROAIRVPIPLNS 352
Db      348 PICROYIRAVHFRS 363

```

```

RESULT 15
US-08-511-485-8
; Sequence 8, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; TITLE OF INVENTION: MAMMALIAN TAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804

```

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/511,485
 FILING DATE: 04-AUG-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 07540/002001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 618 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: both
 MOLECULE TYPE: protein
 US-08-511-485-8

Query Match 7.6%; Score 138.5; DB 1; Length 618;

Best Local Similarity 21.5%; Pred. No. 7e-06;
 Matches 67; Conservative 50; Mismatches 119; Indels 75; Gaps 13;

QY 82 QEVNCKGVIOQLTQEHKMNVRRTTHLNDCKIITHQRTNTPFDLVPHEDGVDAVRV 141
 Db 343 EVDDEIQGRYPHL--EQLISTSDTTGEENADPPIIH-----FGGESSSEDAVMM 391
 QY 142 LKPL--DSVDLGL-----EIVYKRPHSIQSF--TDVIGYISGERPKGIOE---TE 186
 Db 392 NTPVVKSLKEMGFNDLVKQTLTKLTGENYKTVNDIVSALNADEKREBEKQAE 451
 QY 187 EMLKVGATILTVGEL-----VLDN---NSVRLQPP--KQMQYTLSSOD--FD 227
 Db 452 EWASDDLILIRKRMALFQQLTCVLPILDNLKANVINKQEHDI IKQKTQIPLQARBLID 511
 QY 228 SLLOQESSVRLMKYLALVGFATCATLFFILRKQYLORE-----RLRLKQOEFPQE 281
 Db 512 TIWVGNAAPANTFKQCKLEIDSTLYKNLFVDKMKKTIPTEDVSGLSLEQLRLQBE--- 568
 QY 282 HEAQLLSRAKPEDRESLSKACVVCLSFKSCVFLBEGHVCSTECYRALPEPKCPICRO 341
 Db 569 -----RTCKVCMDKEVSVFIFQGHILVQCQC---APSLRKCPICKG 607
 QY 342 AITRVIPLYNS 352
 Db 608 IIKGTVRTFLS 618

Search completed: February 24, 2006, 08:31:00
 Job time : 48 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 24, 2006, 08:22:24 ; Search time 230 Seconds
(without alignments)
1079.765 Million cell updates/sec

Title: US-09-978-360A-437

Perfect score: 1831

Sequence: 1 MESGRPSLQCFILGTSV.....PKKPCICQALTRVPLTNS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1831	100.0	352	2	0969V5 HUMAN
2	1824	99.6	352	2	072431 HUMAN
3	1818	99.3	352	2	0949B5 HUMAN
4	1815	99.1	352	2	0479G8 MACACA
5	1673	91.4	352	2	08VCM5 MOUSE
6	1672	91.3	352	2	08BHF2 MOUSE
7	1667	91.0	352	2	09DCV9 MOUSE
8	1277.5	69.8	353	2	06NTT6 XENLA
9	1145	62.5	352	2	04S6B4 TETNG
10	776	42.4	341	2	05M7X9 BRARE
11	442.5	24.2	338	2	09VZJ9 DROME
12	436	23.8	339	2	0706A1 ANOGA
13	431.5	23.6	206	2	04RV85 TETNG
14	391.5	21.4	283	2	06PBA9 BRARE
15	384.5	21.0	221	2	06AX71 XENLA
16	301	16.4	343	2	08L7N4 ARATH
17	267.5	14.6	338	2	094HV7 ARATH
18	266	14.5	341	2	09LO59 ARATH
19	230.5	12.6	237	2	09SLU0 ARATH
20	201	11.0	383	2	09STH3 ARATH
21	192	10.5	376	2	04VVC9 MEDTR
22	166	9.1	383	2	099KR6 MOUSE
23	166	9.1	381	2	08CIP0 RAT
24	166	9.1	381	2	06AYH3 RAT
25	166	9.1	402	2	070WP2 GIALA
26	165.5	9.0	355	2	04V818 XENLA
27	165.5	9.0	363	2	04V919 BRARE
28	164.5	9.0	262	2	05DC20 SCHIS
29	164.5	9.0	375	2	05E9J6 BOVIN
30	164.5	9.0	382	2	06GN19 XENLA
31	164	9.0	372	2	09H6W8 HUMAN

32	163	8.9	372	2	0969K3 HUMAN	0969K3 homo sapien
33	163	8.9	372	2	05NV17 PONPY	05NV17 pongo pygma
34	163	8.9	372	2	05NV07 PONPY	05NV07 pongo pygma
35	163	8.9	373	2	08NG47 HUMAN	08NG47 homo sapien
36	163	8.9	373	2	05R509 PONPY	05R509 pongo pygma
37	162.5	8.9	727	1	LRSM1 MOUSE	080216 mus musculu
38	160.5	8.8	257	2	0516W9 ENTHI	0516w9 entamoeba h
39	156	8.5	628	2	08UWD2 BRARE	08Uwd2 brachydantio
40	156	8.5	647	2	07TOK2 BRARE	07TOK2 brachydantio
41	156	8.5	654	2	06ZM93 BRARE	06Zm93 brachydantio
42	156	8.5	699	2	09STH2 DROME	09StH2 drosophila
43	155.5	8.5	333	2	04RXJ0 TETNG	04RXJ0 tetradon n
44	155.5	8.5	723	1	LRSM1 HUMAN	06Uw0 homo sapien
45	154.5	8.4	329	2	05BL61 XENTR	05BL61 xenopus tro

ALIGNMENTS

RESULT 1	
0969V5 HUMAN	
ID 0969V5; HUMAN PRELIMINARY; PRT; 352 AA.	
AC 0969V5;	
DT 01-DEC-2001 (TREMblrel. 19, Created)	
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)	
DT 13-SEP-2005 (TREMblrel. 31, Last annotation update)	
DE Hypothetical protein Clorf166 (Hypothetical protein FUJ12875) (Novel protein) (Hypothetical protein DKFZP762M0911).	
DE Name=Clorf166; Synonyms=DKFZP762M0911, FUJ12875, RP11-401M16.2;	
GN ORFNames=RP11-401M16.2-001;	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Euteria; Euarchontoglires; Primates; Catarrhini; Homnidae;	
OC Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE=Brain, and Skin;	
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;	
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.C.,	
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA Diatchenko L., Marnett L., Farmer A.A., Rubin G.M., Hong L.,	
RA Stalcenon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,	
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,	
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,	
RT "Generation and initial analysis of more than 15,000 full-length human	
and mouse cDNA sequences."	
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RP [2]	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE=Skin;	
RX NIH MGC Project;	
RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.	
RP [3]	
RP NUCLEOTIDE SEQUENCE.	
RC TISSUE=Brain;	
RA Strausberg R.	
RP Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.	
RP [4]	
RP NUCLEOTIDE SEQUENCE.	
RA Kimberley A.	
RP Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.	

[5]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Melanoma;
 RC The German cDNA Consortium;
 RG Blum H., Bauerbachs S., Mewes H.W., Weil B., Amid C., Oeanger A.,
 RA Fodor G., Han M., Wilmann S.,
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC014010; AAH14010.1; -; mRNA.
 DR EMBL: BC010101; AAH10101.1; -; mRNA.
 DR EMBL: AL381357; CAH73470.1; -; Genomc-DNA.
 DR EMBL: AL833889; CAD8745.1; -; mRNA.
 DR Kntseml; ENSG00000090432; Homo sapiens.
 DR GO: GO:0004871; F:signal transducer activity; IMP.
 DR GO: GO:0043123; P:positive regulation of I-kappa kinase/NF-k. .; IMP.
 DR InterPro: IPR01841; Znf_RING.
 DR SMART: SM00184; RING_1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR KX Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
 KM SEQUENCE 352 AA; 39800 MW; 6EF2B8BFC1801F CRC64;
 SQ
 Query Match 100.0%; Score 1831; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.3e-129;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MESSGRPSLCQFILLGTTSVVTAALYSYVROKARVSQELKAKKVLGEDIKSLISEAPG 60
 DB 1 MESSGRPSLCQFILLGTTSVVTAALYSYVROKARVSQELKAKKVLGEDIKSLISEAPG 60
 QY 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIRLTQEHKVMWNRTHLMDCKSIHQH 120
 DB 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIRLTQEHKVMWNRTHLMDCKSIHQH 120
 QY 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLEYEKEFHPISIQSFDTVIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLEYEKEFHPISIQSFDTVIGHYISGERPK 180
 QY 181 GIOETEMLKVGATLTGVELVLNDNSVRLQPPKQMGYYLSSQDFSLQROESSVRLM 240
 DB 181 GIOETEMLKVGATLTGVELVLNDNSVRLQPPKQMGYYLSSQDFSLQROESSVRLM 240
 QY 241 KVLALVFGFATCATLFFILRKQYLOEROERLTKQMEBFQEHQAQLLSRAKPEDRESLKS 300
 DB 241 KVLALVFGFATCATLFFILRKQYLOEROERLTKQMEBFQEHQAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKPCICRAITRVIPLVNS 352
 DB 301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKPCICRAITRVIPLVNS 352
 RESULT 2
 Q7Z431 HUMAN
 ID Q7Z431 HUMAN PRELIMINARY; PRT; 352 AA.
 AC Q7Z431;
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Putative NFkB activating protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RA Matsuda A., Suzuki Y., Honda G., Muramatsu S., Matsuzaki O.,
 RA Nagano S., Doi T., Shimotohno K., Harada T., Nishida E., Hayashi H.,
 RT "Large-scale identification and characterization of human genes that
 activate NF-kappaB and MAPK signaling pathways.";
 RT Oncogene 22:3307-3318(2003).
 DR EMBL: AB097015; BAC7368.1; -; mRNA.

DR EMBL: ENSG00000090432; Homo sapiens.
 DR GO: GO:000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0046872; F:metal ion binding; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:000870; F:zinc ion binding; IEA.
 DR GO: GO:001567; P:protein ubiquitination; IEA.
 DR InterPro: IPR01841; Znf_RING.
 DR SMART: SM00184; RING_1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KM Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 352 AA; 39784 MW; 6EF2B8BFC1801F CRC64;
 Query Match 99.6%; Score 1824; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 1.1e-128;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MESSGRPSLCQFILLGTTSVVTAALYSYVROKARVSQELKAKKVLGEDIKSLISEAPG 60
 DB 1 MESSGRPSLCQFILLGTTSVVTAALYSYVROKARVSQELKAKKVLGEDIKSLISEAPG 60
 QY 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIRLTQEHKVMWNRTHLMDCKSIHQH 120
 DB 61 KCVPAVIEGAVRSVKETLNSQFVENCCKGVIRLTQEHKVMWNRTHLMDCKSIHQH 120
 QY 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLEYEKEFHPISIQSFDTVIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLEYEKEFHPISIQSFDTVIGHYISGERPK 180
 QY 181 GIOETEMLKVGATLTGVELVLNDNSVRLQPPKQMGYYLSSQDFSLQROESSVRLM 240
 DB 181 GIOETEMLKVGATLTGVELVLNDNSVRLQPPKQMGYYLSSQDFSLQROESSVRLM 240
 QY 241 KVLALVFGFATCATLFFILRKQYLOEROERLTKQMEBFQEHQAQLLSRAKPEDRESLKS 300
 DB 241 KVLALVFGFATCATLFFILRKQYLOEROERLTKQMEBFQEHQAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKPCICRAITRVIPLVNS 352
 DB 301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKKPCICRAITRVIPLVNS 352
 RESULT 3
 Q9H9B5 HUMAN
 ID Q9H9B5 HUMAN PRELIMINARY; PRT; 352 AA.
 AC Q9H9B5;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Hypothetical protein FLJ12875.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX NUCLEOTIDE SEQUENCE.
 RP PubMed=14702039; DOI=10.1038/ng1285.
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Ii, Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Nishimura K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoisida M., Hottu T.,
 RA Kuusano Y., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiyasu K., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Mueshino K., Yuki H., Ohnima A., Saeki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hisigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Taniguchi A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togeishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs";
 RT Nat. Genet. 36:40-45(2004).
 DR EMBL: AK022937; BAB14317.1; -; mRNA.
 DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0046872; F:metal ion binding; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro: IPR001841; ZnF_RING.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KM Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 352 AA; 39717 MW; C19F150D278C2DA9 CRC64;

Query Match 99.3%; Score 1818; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 3.2e-128;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESSGRPSLCQFILGTTSVTTALYSYVRQKARVSQELKAKVHLGSDLSISEAG 60
 DB 1 MESSGRPSLCQFILGTTSVTTALYSYVRQKARVSQELKAKVHLGSDLSISEAG 60
 QY 61 KCVPAVIEGAVRSYKELTNSQFVENCCKGVQRLTLOSHKWMNRTTHLMDCKSIHOR 120
 DB 61 KCVPAVIEGAVRSYKELTNSQFVENCCKGVQRLTLOSHKWMNRTTHLMDCKSIHOR 120
 QY 121 TMTVPFDLVPHEDGDVAVRVLPKPLDSVDLGLETVYEKHPISQSFDTVIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGDVAVRVLPKPLDSVDLGLETVYEKHPISQSFDTVIGHYISGERPK 180
 QY 181 GIQETEMLKVGATLTGVELVLDNNSVRLQPPKQMGYYLSSQPDLSILOQESSVRLM 240
 DB 181 GIQETEMLKVGATLTGVELVLDNNSVRLQPPKQMGYYLSSQPDLSILOQESSVRLM 240
 QY 241 KVLALVFPATCATLFFILRKQYLOROERLRLKQOEFOEHAOLLSRAKPEDRESLKS 300
 DB 241 KVLALVFPATCATLFFILRKQYLOROERLRLKQOEFOEHAOLLSRAKPEDRESLKS 300
 QY 301 ACVCLISFSCVFLPFCGHVCSCTECYRALPEPKKPCICROAITRVIPLYNS 352
 DB 301 ACVCLISFSCVFLPFCGHVCSCTECYRALPEPKKPCICROAITRVIPLYNS 352

RESULT 4
 Q4R7G8_MACEA PRELIMINARY; PRT; 352 AA.
 ID Q4R7G8; AC Q4R7G8;
 DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
 DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
 DE Testis cDNA, clone: QcSA-15365, similar to human hypothetical protein
 DE FLJ12875 (FLJ12875).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolpus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9541;
 RP NUCLEOTIDE SEQUENCE.
 RP International consortium for macaque cDNA sequencing, analysis;

RT "DNA sequences of macaque genes expressed in brain or testis and its
 RT evolutionary implications";
 RT Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RA NUCLEOTIDE SEQUENCE.
 RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
 RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
 RT "Substitution rate and structural divergence of 5'UTR evolution:
 RT Comparative analysis between human and cynomolgus monkey cDNAs";
 RT Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AB168850; BA000954.1; -; mRNA.
 DR InterPro: IPR001841; ZnF_RING.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KM Hypothetical protein; Metal-binding; Nuclear protein; Zinc;
 KM Zinc-finger.
 SQ SEQUENCE 352 AA; 39827 MW; 4AB6245101E3B0D2 CRC64;

Query Match 99.1%; Score 1815; DB 2; Length 352;
 Best Local Similarity 99.1%; Pred. No. 5.3e-128;
 Matches 349; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MESSGRPSLCQFILGTTSVTTALYSYVRQKARVSQELKAKVHLGSDLSISEAG 60
 DB 1 MESSGRPSLCQFILGTTSVTTALYSYVRQKARVSQELKAKVHLGSDLSISEAG 60
 QY 61 KCVPAVIEGAVRSYKELTNSQFVENCCKGVQRLTLOSHKWMNRTTHLMDCKSIHOR 120
 DB 61 KCVPAVIEGAVRSYKELTNSQFVENCCKGVQRLTLOSHKWMNRTTHLMDCKSIHOR 120
 QY 121 TMTVPFDLVPHEDGDVAVRVLPKPLDSVDLGLETVYEKHPISQSFDTVIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGDVAVRVLPKPLDSVDLGLETVYEKHPISQSFDTVIGHYISGERPK 180
 QY 181 GIQETEMLKVGATLTGVELVLDNNSVRLQPPKQMGYYLSSQPDLSILOQESSVRLM 240
 DB 181 GIQETEMLKVGATLTGVELVLDNNSVRLQPPKQMGYYLSSQPDLSILOQESSVRLM 240
 QY 241 KVLALVFPATCATLFFILRKQYLOROERLRLKQOEFOEHAOLLSRAKPEDRESLKS 300
 DB 241 KVLALVFPATCATLFFILRKQYLOROERLRLKQOEFOEHAOLLSRAKPEDRESLKS 300
 QY 301 ACVCLISFSCVFLPFCGHVCSCTECYRALPEPKKPCICROAITRVIPLYNS 352
 DB 301 ACVCLISFSCVFLPFCGHVCSCTECYRALPEPKKPCICROAITRVIPLYNS 352

RESULT 5
 O8VCMS_MOUSE PRELIMINARY; PRT; 352 AA.
 ID O8VCMS; AC O8VCMS;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE RIKEN cDNA 0610009K11.
 GN Name=0610009K11.rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RP STRAIN=FVB/N; TISSUE=Liver;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019516; AAH19516.1; -. mRNA.
 DR HSSP; P38398; 1.M7.
 DR Ensembl; ENSMUSG0000041241; Mus musculus.
 DR MGI; MGI:1915600; 0610009K11R1K.
 DR GO; GO:0016021; C:Integral to membrane; TAS.
 DR InterPro; IPR001841; Znf_RING.
 DR SMART; SMO0184; RING_1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 352 AA; 39821 MW; F3FE5D4771E0B140 CRC64;
 Query Match 91.4%; Score 1673; DB 2; Length 352;
 Best Local Similarity 90.1%; Pred. No. 2.5e-117;
 Matches 317; Conservative 18; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MESGGRSLCOFILGTTSTVTAALVYVYRKARVSGELKARKVHLGDLKSLSEAP 60
 DB 1 MESSGRSLCOVILLGTTSSWTAVLVYSYRKQAVDELKAKKHLGDLKSLSEAP 60
 QY 61 KCVYAVIEGAVSVKKTLSQFVENCXGYORLTQEHGMVNRTHLMNDSKTIHOR 120
 DB 61 KCVYAVIEGAVSVKKTLSQFVENCXGYORLTQEHGMVNRTHLMNDSKTIHOR 120
 QY 121 TNYVPLVPHEDGVDAVAVLKLPSVDLGLSTVYEKFPSSIOSEFVDVIGHYISGERPK 180
 DB 121 TNYVPLVPHEDGVDAVAVLKLPSVDLGLSTVYEKFPSPVOSTLDAIGHYISGERPK 180
 QY 181 GIOETEMKLVGATLTGVEGLVLDNNSVRLQPRKQMOYLLSSQDPSLLQROESSVRLM 240
 DB 181 GIOETEMKLVGATLTGVEGLVLDNNAVRLQPRKQMOYLLSSQDPSLLHROESSVRLM 240
 QY 241 KVLALVGFATCATLFFILRKQYLQROERLRLKQMOEFOEHRALQLLSRAKPEDRESLKS 300
 DB 241 KVLALVGFATCATLFFILRKQYLQROERLRLQOOLQEPLEHNAQLLSQASPEDRESLKS 300
 QY 301 ACVVCSSPFSKCVFLGEGHVCSTECYRALPEPKPCPIRQATRVYIPLYNS 352
 DB 301 ACVVCSSPFSKCVFLGEGHVCSCROCYALPEPKPCPIRREITRVYIPLYNS 352
 Db ACVVCSSPFSKCVFLGEGHVCSCROCYALPEPKPCPIRREITRVYIPLYNS 352
 RESULT 6
 Q8BHF2_MOUSE PRELIMINARY; PRT; 352 AA.
 AC Q8BHF2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
 DE library, clone:A830089D08 product:hypothetical RING finger containing
 DE protein, full insert sequence (Mus musculus 0 day neonate head cDNA,
 DE RIKEN full-length enriched library, clone:4831423H02
 DE product:hypothetical RING finger containing protein, full insert
 DE sequence) (Mus musculus adult male liver tumor cDNA, RIKEN full-length
 DE enriched library, clone:C730031H18 product:hypothetical RING finger
 DE containing protein, full insert sequence).
 GN Name=0610009K11R1K;
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehi Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cavaant T.,
 RA Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfield D., Boujnea N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gaitanaris M.,
 RA Gasteirich S., Hill D., Hofmann W., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima Y., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
 RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 403:685-690 (2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Oseato N., Saito R., Suzuki H., Yamanka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schenbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kannin A., Matsuda H., Batalov S., Beisler K.W.,
 RA Blake J., Bradt D., Brusic V., Choehia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Glass C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlee G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takekida Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszew-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai U., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=cortex, Head, and Liver;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RX Shihata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa E., Ohara E., Wachihi M.,
 RA Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsuzawa S., Kawai J.,
 RA Kameda Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shihata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Toyota T., Yasunishi A., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 [7]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Liver;
 RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shihata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Toyota T., Yasunishi A., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 [8]
 RN NUCLEOTIDE SEQUENCE.
 RC EMBL; AK076419; BAC36332.1; -; mRNA.
 RC EMBL; AK083295; BAC3848.1; -; mRNA.
 DR HSPB, P38398, JMW.
 DR Ensemble; ENSMUSG0000041241; Mus musculus.
 DR MGI; MGI:1915600; 0610009K1ir1k.
 DR GO; GO:0016021; C.integral to membrane; TAS.
 DR InterPro; IPR001841; ZNF_RING.
 DR SMART; SM00184; RING_1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 DR Hypothetical protein; Metal-binding; Zinc; zinc-finger.
 KW SEQUENCE 352 AA; 39835 MW; 252530F1BD917871 CRC64;
 SQ

Query Match 91.3%; Score 1672; DB 2; Length 352;
 Best Local Similarity 89.8%; Pred. No. 3e-117;
 Matches 316; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MESSGSPSICQFLLCTSVTAATSVYRQKARVSOELGKAKVHIGEDLSITSEARG 60
 DB 1 MESSGSPSICQVLLTSSMTAVLSITRQKQVAGELGKAKHILGEDIKILSEARG 60
 QY 61 KCVPYAVIGAVRSVKEITNSQFVENCQGVIOQLTQEHKMWNRTHLMDCKSIHOR 120
 DB 61 KCVPYAVIGAVRSVKEITNSQFVENCQGVIOQLTQEHKMWNRTHLMDCKSIHOR 120

QY 121 TMTVPFDLVPHEDGVAVRVLKPLDSYDLGLFETVEKFKHPSIOSFTVDIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGVAVRVLKPLDSYDLGLFETVEKFKHPSIOSFTVDIGHYISGERPK 180
 QY 181 GIQTEEMLKVGATLTGVGELVLDNNSVRLQPPKQGMQYIYSSQDFSLQROESSVRLW 240
 DB 181 GIQTEEMLKVGATLTGVGELVLDNNSVRLQPPKQGMQYIYSSQDFSLQROESSVRLW 240
 QY 241 KYLALVFGFATCATLFFILRRQYLOROERLKLKQOEFOHEHQLSRAPDEBSLKS 300
 DB 241 KILVAVFPAFCATLFFILRRQYLOROERLKLKQOEFOHEHQLSRAPDEBSLKS 300
 QY 301 ACVCLSNFKSCVFLFECGHVCSCTECYALPEPKPCPIROAITVEIPLVNS 352
 DB 301 ACVCLSNFKSCVFLFECGHVCSCTECYALPEPKPCPIROAITVEIPLVNS 352

RESULT 7
 Q9DCV9 MOUSE
 ID Q9DCV9 MOUSE PRELIMINARY; PRT; 352 AA.
 AC Q9DCV9
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mus musculus adult male kidney cDNA, RIKEN full-length enriched
 DE library, clone:0610009K1 product:hypothetical RING finger containing
 DE protein, full insert sequence.
 GN Name=0610009K1R1k;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RX Kawai J., Shingawa A., Shihata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita K., Gariboldi M.,
 RA Guernicich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Momberts P.,
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shihata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 403:685-690(2001).
 [3]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RL Nature 420:563-573(2002).
 [4]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20499374; PubMed=11042119; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama Y., Nishi K., Kitesuna T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada K.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Ozawa K., Tanaka T., Matsumura S., Kawai Y.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai Y.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi Y., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imocani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai Y., Kojima Y., Kono H., Konda M., Koya S., Kurihara C.,
RA Matsumura T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Tejima Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (Jul-2000) to the EMBL/GenBank/DBD databases.
DR EMBL; AK002416; BAB22084.1; -; mRNA.
DR HSSP; P38338; 1M7.
DR Ensembl; ENSMUSG00000041241; Mus musculus.
DR MGI; MGI:1915609; 0610009K1Rik.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001841; znf_RING.
DR SMART; SM00184; RING_1.
DR PROSITE; PS50089; ZF_RING_2, 1.
DR KEGG; H00000; Zinc finger, Metal-binding; Zinc, zinc-finger.
SQ HYPOTHECAL protein; 352 AA; 39883 MW; 299333d6BD9165c6 CRC64;
SC SEQUENCE

Query Match 91.0%; Score 1667; DB 2; Length 352;
Best Local Similarity 89.5%; Pred. No. 7,1e-117;
Matches 315; Conservative 19; Mismatches 18; Indels 0; Gaps 0

QY 1 MESGRPSICQFILLIGTTSVVTAAIYSVYRQARVSOELKAKKVIHGEDLSILSEAPG 60
DB 1 MESGRSPISGGVILLIGTSSMTAVAIYSIYRKAQVAQELGKAKIHLGEDLIGTILSEAPG 60
QY 61 KCVPAVAVLEGARVSKETILNSQFVNCCKGVIGRLTIOEHKVMWNRTHTHMNCSTKIHOR 120
DB 61 KCVPAVAVLEGARVSKETILNSQFVNCCKGVIGRLTIOEHKVMWNRTHTHMNDYSKTIHOR 120
QY 121 TNTVPFDIVPHEDGVAVRVLAKPLDSVDLGLGTVEYKHPHSIOSFTDVIYGHYISGERPK 180
DB 121 TINTVPFDIVPHEDGVAVRVLAKPLDSVDLGLGTVEYKHPHSIOSFTDVIYGHYISGERPK 180
QY 181 GIQETFEMLKYGATITGIGELVLDNNSVRLQPPKQGMQYIYSSQDFDSTLQRESSVRLM 240
DB 181 GIQETFEMLKYGATITGIGELVLDNNSVRLQPPKQGMQYIYSSQDFDSTLQRESSVRLM 240
QY 241 KVLAVLFPFACATLFTILRKQYLROEELRLKMOEERQOEHAQLLSAKRPEDESLKS 300
DB 241 KVLAVLFPFACATLFTILRKQYLROEELRLKMOEERQOEHAQLLSAKRPEDESLKS 300
QY 301 ACVVCCLASSFKSCVFLGCGHVCCTCEYRALPEPKPCPTICORALITVPIPLVNS 352

301 ACVCTLSNFKSCVFLECGHVCSCRCYIALPEPKRCPICRRTTRIVIPLYNS 352

Db

RESULT 8

Q6NTT6_XENLA PRELIMINARY; PRT; 353 AA.

ID Q6NTT6; 05-JUL-2004 (Tremblrel. 27, Created)

AC Q6NTT6; 05-JUL-2004 (Tremblrel. 27, Last sequence update)

DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DE MGCC2282 protein.

OS Name=MGCC2282;

OS Xenopus laevis (African clawed frog).

OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.

NCBI_Taxid=8335;

[1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Scheef C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultx S.W.,

RA Villalon D.K., Nuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madcan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shechenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield V.S.N., Krzywinski M.T., Skalska U., Smalusz D.E.,

RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RL and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Kidney;

RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;

RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

RL initiative."

RL Dev. Dyn. 225:384-391(2002).

[3]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Kidney;

RX Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.

CC EMBL: BC068863; AA068863.1; -; mRNA.

DR EML: BC068863; AA068863.1; -; mRNA.

DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.

DR GO: GO:0046872; F:metal ion binding; IEA.

DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.

DR GO: GO:0008270; F:zinc ion binding; IEA.

DR GO: GO:0001657; P:protein ubiquitination; IEA.

DR InterPro: IPR001841; Znf_RING.

DR Pfam: PF00097; zf-C3HC4_1.

DR SMART: SM00184; RING; 1.

DR PROSITE: PS50089; ZF_RING_2; 1.

KW Metal-binding; Ub1 conjugation pathway; Zinc; Zinc-finger.

SQ SEQUENCE 353 AA; 40359 MW; 102A3C761CD07EFA CRC64;

Query Match 69.8%; Score 1277.5; DB 2; Length 353;

Best Local Similarity 64.9%; Pred. NO. 1.3e-87;

Matches 223; Conservative 63; Mismatches 60; Indels 1; Gaps 17;

QY 1 MESSGRPSLCOPILIGTTSTVTAALYSYVYRORAKARYSOELKGAKVHLGEDLSILSEARG 60
 Db 1 MESSGRPSVGVVILITTSATLALFYSTRHRYKRVQTLKEAKFCLTDLDLPAVLSDBPG 60
 QY 61 KCPVPAVIEGAVRSVYKELTNSQFVENCCKGVIOQLTLOEHKVMWNRTHLMDNSCKIIHOR 120
 Db 61 KCPVPAVIEGAVRSVYKELTNSQFVENCCKGVIOQLTLOEHKVMWNRTHLMDNSCKIIHOR 120
 QY 121 TMTVPFDLVPHEDGVN-VAVRYLKPIDSVDLGLETYKEKPHPSIQSFDTVIGHYIGSERP 179
 Db 121 TMTVPFDLVPHEDGVN-VAVRYLKPIDSVDLGLETYKEKPHPSIQSFDTVIGHYIGSERP 180
 QY 180 KGIOEEMKLVKATLTGVGELVDNNSVRLPPKQOMGYLSSQOPDLSLQROESSVRL 239
 Db 181 KGIOEEMKLVKATLTGVGELVDNNSVRLPPKQOMGYLSSQOPDLSLQROESSVRL 240
 QY 240 KVALVFPFATCATLFTFLRKQYLOQRORLRLKQOEFOEHEAQLSRAPKEDRESLKS 299
 Db 241 RLTLSTLFGAACSTLFTFLMRLYQHRRSRKERSVLEBPAAQOKRLBLNVDESCLSPS 300
 QY 300 SACVCLSFKSCVFLFEGCHVCSCTECYRALPEPKKCPICRAITVPIPLNS 352
 Db 301 VCSICLSRORSQVFLFEGCHVCSCTECYRALPEPKKCPICRAITVPIPLNS 353
 RESULT 9
 QAS6B4_TETNG PRT; 352 AA.
 ID QAS6B4_TETNG PRELIMINARY;
 AC QAS6B4;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Chromosome 9 SCAR14729, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00023363001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodon.
 OC NCBI_TaxId=99883;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 RA Jallou O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Oufou-Costat C., Bernot A.,
 RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Catolico L., Poulin J., De Bernardis V.,
 RA Crnaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schacher V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolious H.,
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RA the early vertebrate proto-laryotype".
 RA Nature 431:946-957(2004).
 RN [2]
 RA NUCLEOTIDE SEQUENCE.
 RA Genoscope, Whitehead Institute Centre for Genome Research;
 RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB01014729; CAG03818.1; -; Genomic_DNA.
 FT NON TER 352 352 82P8A5E08C538F4 CRC64;
 SQ SEQUENCE 352 AA; 39686 MM; 82P8A5E08C538F4 CRC64;
 Query Match 62.5%; Score 1145; DB 2; Length 352;
 Best Local Similarity 59.4%; Pred. No. 1.2e-77;
 Matches 209; Conservative 55; Mismatches 88; Indels 0; Gaps 0;

QY 1 MESSGRPSLCOPILIGTTSTVTAALYSYVYRORAKARYSOELKGAKVHLGEDLSILSEARG 60
 Db 1 MESSGRPSVGVVILITTSATLALFYSTRHRYKRVQTLKEAKFCLTDLDLPAVLSDBPG 60
 QY 61 KCPVPAVIEGAVRSVYKELTNSQFVENCCKGVIOQLTLOEHKVMWNRTHLMDNSCKIIHOR 120
 Db 61 KCPVPAVIEGAVRSVYKELTNSQFVENCCKGVIOQLTLOEHKVMWNRTHLMDNSCKIIHOR 120
 QY 121 TMTVPFDLVPHEDGVN-VAVRYLKPIDSVDLGLETYKEKPHPSIQSFDTVIGHYIGSERP 180
 Db 121 TMTVPFDLVPHEDGVN-VAVRYLKPIDSVDLGLETYKEKPHPSIQSFDTVIGHYIGSERP 180
 QY 180 KGIOEEMKLVKATLTGVGELVDNNSVRLPPKQOMGYLSSQOPDLSLQROESSVRL 240
 Db 181 KGIOEEMKLVKATLTGVGELVDNNSVRLPPKQOMGYLSSQOPDLSLQROESSVRL 240
 QY 241 KVALVFPFATCATLFTFLRKQYLOQRORLRLKQOEFOEHEAQLSRAPKEDRESLKS 300
 Db 241 RLTLSTLFGAACSTLFTFLMRLYQHRRSRKERSVLEBPAAQOKRLBLNVDESCLSPS 300
 QY 300 SACVCLSFKSCVFLFEGCHVCSCTECYRALPEPKKCPICRAITVPIPLNS 352
 Db 301 VCSICLSRORSQVFLFEGCHVCSCTECYRALPEPKKCPICRAITVPIPLNS 352
 RESULT 10
 QSM7X9_BRARE PRT; 341 AA.
 ID QSM7X9_BRARE PRELIMINARY;
 AC QSM7X9;
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Hypothetical protein zgc:92166.
 DE ORFNames=zgc:92166;
 GN Brachydanio rerio (Zebrafish) (Danio rerio).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxId=7955;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 RA TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Scheenen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Uebin T.B., Toshitoki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fanny J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RA and mouse cDNA sequences".
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RA NUCLEOTIDE SEQUENCE.
 RA TISSUE=Whole;
 RC NIH MGC Project;
 RC Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC088385; AA88385.1; -; mRNA.
 DR EMBL; ENSDARG0000021398; Danio rerio.
 DR ZFIN; ZDB-GENE-050102-5; zgc:92166.
 GO; GO:0000151; Cytidylate ligase complex; IEA.

DR GO:0046872; F-metal ion binding; IEA.
 DR GO:0004842; F-ubiquitin-protein ligase activity; IEA.
 DR GO:0008270; F-zinc ion binding; IEA.
 DR GO:0015557; F-protein ubiquitination; IEA.
 DR InterPro: IPR001841; ZnF_RING.
 DR PROSITE: P550089; ZF_RING.
 DR Hypothetical protein; Metal-binding; Nuclear protein; Zinc;
 KW Zinc-finger.
 SQ SEQUENCE 341 AA; 38585 MW; 4807666981CFD70 CXC64;

Query Match 42.4%; Score 776; DB 2; Length 341;
 Best Local Similarity 43.9%; Pred. No. 6.3e-50;
 Matches 151; Conservative 72; Mismatches 109; Indels 12; Gaps 5;

QY 11 QPILGTSVVAALAYSVYRQKARVSOELKGAQVHIGEDKSLSEAPGCVAYVIEG 70
 DB 8 EAVCGSSVALSGLFYIRKRRKVDKAPVWALDAKIDILNTPGCIQYVVEG 67
 QY 71 AVRSVKEITLNSQFVENCQVIGIQLTQEHKVMNRTHLNMDCSKIIHQRTNTPDLPV 130
 DB 68 TVQPVGEPLRSQFQSSVGVIGKLVREHKLVNMSLGRITWDSRVILQRNANVPFNL- 126
 QY 131 HEDGVDA-VVILKPLDSVDGLFVYKRPISQSFIDYGHYISGPRKGIQETEMT 189
 DB 127 ---GLNKFVAVLCPELATGPKMEIVHKFHQATYVGTDLIGQYLSGKPKQLETEM 183
 QY 190 KVAGATLTVGELVLDNNS-VRLQPPKQMGQYTLSSQFDSLQROESSVRLMKVLAIFG 248
 DB 184 KVGASLTVVGGELIDTDLRLKIRPPTGSEVFLLSNAPETILMEQEQAVRWVAFICA 243
 QY 249 FATATLFFILRKQYLQREKLRLKQOEQEHQALSLRANREDRSIKSAQVCLSS 308
 DB 244 LAGVAVLWTRRRYRQKLRMEQENLREREG----MGTEGEEDNGVENACVICLSN 298
 QY 309 FKSCVFLCGHVCCTEYRALPEPKKCPICROAITVPIVLYNS 352
 DB 299 PRGCVLLDCGHVCCFCFYQALRPP-FCPICRHKKRVLEPLV 341

RESULT 11
 Q9VZJ9 DROME
 ID Q9VZJ9 DROME PRELIMINARY; PRT; 338 AA.
 AC Q9VZJ9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE CG1134-PA (AT15655D).
 GN ORNames=CG1134, CG1134;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1]
 NP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20186006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananthanides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Panicoch C., Baldwin D.,
 RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu U., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotilier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dudson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klanos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 NP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568.
 RA Celnikier S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svitzkas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RL melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
 RN [3]
 NP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svitzkas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.B., Rubin G.M.,
 RA Ashburner M., Celnikier S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RL a genomes perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
 RN [4]
 NP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mitra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu U., Berman B.P.,
 RA Bettencourt B.R., Celnikier S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 RN [5]
 NP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celnikier S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svitzkas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 NP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RA Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RN [7]
 NP NUCLEOTIDE SEQUENCE.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guatin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,

RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celinker S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- INTERACTION: NDBExp-1, IntAct-EBI-156824, EBI-174493;
 CC Q9V57:act; NDBExp-1, IntAct-EBI-156824, EBI-174493;
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL; AE003480; AAF47822.1; -; Genomic_DNA.
 DR EMBL; AY113263; AAM29268.1; -; mRNA.
 DR Intact; Q9VZJ9; -;
 DR Ensemble; CG1134; Drosophila melanogaster.
 DR Flybase; FBgn0035483; CG1134.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0000151; C:cubiquitin ligase complex; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:001567; P:protein ubiquitination; IEA.
 DR InterPro; IPR001841; Znf_RING.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PSS0089; ZF_RING_2; 1.
 DR Metal-binding; Ubl conjugation pathway; Zinc; Zinc-finger.
 DR KW Metal-binding; Ubl conjugation pathway; Zinc; Zinc-finger.
 DR SQ SEQUENCE 338 AA; 3784 MW; FD882A3020517AD2 CRC64;
 Query Match 24.2%; Score 442.5; DB 2; Length 338;
 Best Local Similarity 30.6%; Pred. No. 7.2e-25;
 Matches 104; Conservative 74; Mismatches 143; Indels 19; Gaps 8;
 QY 9 LCQFILGTTSVTAALYSVYRQKARVSOELKGAKVHLGEDIKSLSEAPGKCVYAVI 68
 DB 4 LHEAVLGLDILVVCSSNQYKLRKNCRLKADAPQLQDDPLADRLRKEPQKLYAVI 63
 QY 69 EGAIVSVKETSLSQFVENCQVYQRLTLOEHKVMNRTTHLWDSCKIIHQTNTVPDL 128
 DB 64 RGSVTPIGTALRSASPSVTVGLQTMLTLEHR-VARAMEGFQOEKQIIVHSANETPFEL 122
 QY 129 VHEHDGVAVAVKPLDSVDGLFTVYEKHPHSIQSFVDVGHYISGERPKGIQETEM 188
 DB 123 VNGKQGVV---IVGSLSELDMDVYENPSSLTVPDHLFGLPSGVQGLQTTTEV 178
 QY 189 LKVGATLTGVLGVLDNNSVRLQPPKQMGQVYLSQDFPSLLQROESSVRLMKVLAIVFG 248
 DB 179 LRGSGFLTAIGLELDLDTLRMQPSNEG-PLFLTAFTKSTLIRPFDA-KTTTILTV-- 234
 QY 249 FATCATL-----FFILRKQYLOERLRLKQMOEFOEHEAQLLSRAKEDRESLSKACY 303
 DB 235 --VCSFTISAILVAFIKKLYRKRKQREERAKIRERLTERERRARRSRPHTL-SQDQLCV 291
 QY 304 VCLSSFKSCVPLECGVCSCTECYRALPEPKKPCICROAI 343
 DB 292 VCSINPKETITLLPCGHVCLCECAQKI--SVTCPCVGRGSI 329
 RESULT 12
 ID OT06AI ANOGA PRELIMINARY; PRT; 339 AA.
 AC OT06AI;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE ENSANGP0000010763.
 GN ORFNames=ENSANG00000008274;
 OS Anopheles gambiae str. FESST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_Taxid=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AA801008960; RA11729.1; -; Genomic_DNA.
 DR GO; GO:0000151; C:cubiquitin ligase complex; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:001567; P:protein ubiquitination; IEA.
 DR InterPro; IPR001841; Znf_RING.
 DR PROSITE; PSS0089; ZF_RING_2; 1.
 DR Metal-binding; Zinc; Zinc-finger.
 DR KW Metal-binding; Zinc; Zinc-finger.
 DR SQ SEQUENCE 339 AA; 38041 MW; 7B8C659E2F215873 CRC64;

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AA801008960; RA11729.1; -; Genomic_DNA.
 DR GO; GO:0000151; C:cubiquitin ligase complex; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:001567; P:protein ubiquitination; IEA.
 DR InterPro; IPR001841; Znf_RING.
 DR PROSITE; PSS0089; ZF_RING_2; 1.
 DR Metal-binding; Zinc; Zinc-finger.
 DR KW Metal-binding; Zinc; Zinc-finger.
 DR SQ SEQUENCE 339 AA; 38041 MW; 7B8C659E2F215873 CRC64;
 Query Match 23.8%; Score 436; DB 2; Length 339;
 Best Local Similarity 31.5%; Pred. No. 2.2e-24;
 Matches 107; Conservative 67; Mismatches 148; Indels 18; Gaps 6;
 QY 9 LCQFILGTTSVTAALYSVYRQKARVSOELKGAKVHLGEDIKSLSEAPGKCVYAVI 68
 DB 4 LQEAIVLGLDILVVCSSNQYKLRKNCRLKADAPQLQDDPLADRLRKEPQKLYAVI 63
 QY 69 EGAIVSVKETSLSQFVENCQVYQRLTLOEHKVMNRTTHLWDSCKIIHQTNTVPDL 128
 DB 64 RGSVTPIGTALRSASPSVTVGLQTMLTLEHR-VARAMEGFQOEKQIIVHSANETPFEL 122
 QY 129 VHEHDGVAVAVKPLDSVDGLFTVYEKHPHSIQSFVDVGHYISGERPKGIQETEM 188
 DB 123 VNGKQGVV---IVGSLSELDMDVYENPSSLTVPDHLFGLPSGVQGLQTTTEV 178
 QY 189 LKVGATLTGVLGVLDNNSVRLQPPKQMGQVYLSQDFPSLLQROESSVRLMKVLAIVFG 248
 DB 179 LRGSGFLTAIGLELDLDTLRMQPSNEG-PLFLTAFTKSTLIRPFDA-KTTTILTV-- 234
 QY 249 FATCATL-----FFILRKQYLOERLRLKQMOEFOEHEAQLLSRAKEDRESLSKACY 303
 DB 235 --VCSFTISAILVAFIKKLYRKRKQREERAKIRERLTERERRARRSRPHTL-SQDQLCV 291
 QY 304 VCLSSFKSCVPLECGVCSCTECYRALPEPKKPCICROAI 343
 DB 292 VCSINPKETITLLPCGHVCLCECAQKI--SVTCPCVGRGSI 329
 RESULT 13
 ID Q4RV85 TETNG PRELIMINARY; PRT; 206 AA.
 AC Q4RV85;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DE 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Chromosome 15 SCAFL492, whole genome shotgun sequence.
 GN ORFNames=GSTENG00028458001;
 OS Tetradon nigrivittatus (Green puffer).
 OC Tetradon nigrivittatus (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetradontiformes;
 OC Tetradontidae; Tetradontidae; Tetradont.
 OX NCBI_Taxid=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozout-Costaz C., Bernot A.,
 RA Nicolas S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Caetelli V., Katinka M., Vacherie B.,
 RA Bismont C., Skalli Z., Catellico L., Poullain J., De Bernardis V.,
 RA Crnaud C., Duprat S., Broctier P., Coutanceau J.P., Guzy J.,
 RA Parra G., Lardier G., Chaple C., McKernan K.J., McEwan P., Bosak S.,

RA Kellis M., Volf J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lander V., Schachter V., Queller F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope, Whitehead Institute Centre for Genome Research;
 RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL: CA60104992; CAG07697.1; -, Genomic_DNA.
 DR InterPro: IPR001841; Znf_RING.
 DR Pfam: PF00097; ZF-C3HC4_1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Metal-binding; Nuclear protein; Ub1 conjugation pathway; Zinc;
 KW Zinc-finger.
 SQ SEQUENCE 206 AA; 23238 MW; FC2F07246247B46E CRC64;

Query Match 23.6%; Score 431.5; DB 2; Length 206;
 Best Local Similarity 41.0%; Pred. No. 2.6e-24;
 Matches 84; Conservative 44; Mismatches 70; Indels 7; Gaps 3;
 QY 152 LETYVEKHPISIOFTDVIIGHYISGRPKIOETHEMLKYGATLTGVEGLVLDNNSVRL 210
 DB 1 MEMIHEKHFQVSSGLVIVQYISGSEPKQGLTEHEMLKVGALVIGAGELVLAADGTL 60
 QY 211 QPPKQMGQYIISODPDSLLORESSVRLKVLAVGFATCATLPEILKQYLOQERL 270
 DB 61 QPSPDGSEYPLSLVDVPSLQGLKSAVWCWMLAVSALIGTAVLVWVCRRYCHKAKR 120
 QY 271 RLKMOSEFOHEHAKQLSPRAKPED----RESLSKSAQVYVLSFPKSCVFLKCHVSCIE 325
 DB 121 QLEERKIFERMSEPRVRLSPQASVNLVEQVENICVLCYTERNCIIMDCGHVCCCVS 180
 QY 326 CYRALPEPKKCPICQAIITRVPILY 350
 DB 181 CYQALVQ-RKCPICQDISRVPLH 204

RESULT 14
 O6PBA9_BRAE
 ID O6PBA9_BRAE PRELIMINARY; PRT; 283 AA.
 AC O6PBA9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE LOC402879 protein (Fragment).
 GN Name=LOC402879;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dlatchenko L., Matovina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC059797; AAH59797.1; -, mRNA.
 FT NON TER 1
 SQ SEQUENCE 283 AA; 31798 MW; CD3C66BB7B68350C CRC64;

Query Match 21.4%; Score 391.5; DB 2; Length 283;
 Best Local Similarity 37.2%; Pred. No. 3.9e-21;
 Matches 92; Conservative 45; Mismatches 103; Indels 7; Gaps 5;
 QY 13 ILGTTSTVYTAALYSVTRQKARVSGELGAKKVLHGEDLSLSAPKCVYAVIEAV 72
 DB 25 IAGSCFAPSGFLYTLSDKRLKELIPFQPDHLLILNNSKRLHYAVAEGLV 84
 QY 73 RSVKETLSQYENCKGVIOQLTLOEHKVMNRTHLWNSDKLIH--QRTNTVPFDLV- 129
 DB 85 QAVGPISISOYVPRCHGVIOKITVHEHKNYSLLKSW--VSKYNNQQTNTVPTFLVQ 142
 QY 130 PHEDGVAVVYLRKLDSDVDLGLFVYKFPSPISQSFVDVGHYISGRPRGIOETEML 189
 DB 143 POSFSDVCARVDSPLESGPFLQQVHRVNAEGLDAVLGEISGKPTALEEREDLL 202
 QY 190 KVGATLTGVEGLVLDNNSV-RLQPPKQMGQYIISODPDSLLORESSVRLKVLAVGF 248
 DB 203 RVGVPLTAFGEIVLEQEKIMRIQPPKQGRSVLLPSDYNSMQHNSVNMKGLTVLFG 262
 QY 249 FATCATL 255
 DB 263 L-TGSTL 268

RESULT 15
 O6AX71_XENLA
 ID O6AX71_XENLA PRELIMINARY; PRT; 221 AA.
 AC O6AX71;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE MGC83539 protein.
 GN Name=MGC83539;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oocytes;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oocytes;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Rana S.S., Ligonellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Paley J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gittwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalski S., Smalhus D.E.,
 RA Schmecher A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."; *Proc. Natl. Acad. Sci. U.S.A.* 99:16899-16903 (2002).
 RN [3].
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oocytes;
 RA Klein S., Gerhard D.S.;
 RL Submitted (AUG-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC079729; AAH79729.1; -, mRNA.
 SO SEQUENCE 221 AA, 2458 MW, 1BBF4C4B3AC08A9A CMC64;

Query Match	21.0%;	Score 384.5;	DB 2;	Length 221;
Best Local Similarity	39.0%;	Pred. No. 9.6e-21;		
Matches 80;	Conservative 48;	Mismatches 70;	Indels 7;	Gaps 4

[illegible]

Search completed: February 24, 2006, 08:29:23
Job time : 233 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 24, 2006, 08:25:44 ; Search time 41 Seconds
(without alignments)
826.056 Million cell updates/sec

Title: US-09-978-360A-437

Perfect score: 1831

Sequence: 1 MESSGRPLCQFLLIGTTSV.....PKKPCICQATRVIPLYNS 352

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230.5	12.6	237	2	T52432
2	201	11.0	383	2	P96582
3	138.5	7.6	115	2	B96664
4	138.5	7.6	618	2	S68450
5	137.5	7.5	604	2	S68449
6	136.5	7.5	316	2	T32659
7	134.5	7.3	428	2	T48167
8	131.5	7.2	358	2	JCS964
9	130	7.1	943	2	S68824
10	124.5	6.8	200	2	A96664
11	123	6.7	275	2	A45679
12	121.5	6.6	124	2	T01251
13	118	6.4	286	2	D36828
14	118	6.4	824	2	T14172
15	117.5	6.4	824	2	T16028
16	116.5	6.4	268	2	T10304
17	116.5	6.4	268	2	A53989
18	116.5	6.4	299	2	T45881
19	116	6.3	433	2	UC7678
20	115.5	6.3	739	2	E86434
21	115	6.3	497	2	S69545
22	112.5	6.1	288	2	D97113
23	112.5	6.1	522	2	T18504
24	112	6.1	275	2	T10110
25	112	6.1	496	2	S68452
26	111	6.1	401	2	G96824
27	110.5	6.0	337	2	T48341
28	110	6.0	754	2	S35503
29	110	6.0	797	2	AH1674

30	107.5	5.9	529	2	T19204	hypothetical prote
31	107.5	5.9	753	2	S35371	finger protein neu
32	106.5	5.8	106	2	T10212	hypothetical prote
33	106.5	5.8	1133	1	S41478	DNA repair protein
34	105.5	5.8	234	2	T30427	probable apoptotic
35	105.5	5.8	489	2	T26069	hypothetical prote
36	104.5	5.7	202	2	T04906	hypothetical prote
37	104.5	5.7	780	2	T31548	hypothetical prote
38	104.5	5.7	823	2	D86165	protein p15K9.3 li
39	103.5	5.7	936	2	E71405	probable ankyrin -
40	103	5.6	711	2	C84767	hypothetical prote
41	102.5	5.6	1403	2	T17372	plasma membrane-as
42	102	5.6	132	2	B85092	hypothetical prote
43	102	5.6	797	2	AH1302	primosomal replica
44	100.5	5.5	131	2	T41790	AcNMPV orf44 - Bom
45	99.5	5.4	131	2	D72855	AcOrf-44 protein -

ALIGNMENTS

RESULT 1

T52432 hypothetical protein ZCF61 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004

C:Accession: T52432

R:Kato, A.; Suzuki, M.; Kuwahara, A.; Ooe, H.; Higano-Inaba, K.; Komeda, Y.

Gene 239, 309-316, 1999

A>Title: Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana genomic reg

A:Reference number: 225171

A:Accession: T52432

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-217 <KAT>

A:Cross-references: UNIPROT:Q9SLU0; UNIPARC:UPI00000A3331; EMBL:AB028228; P1DN:BA07953.

A:Experimental source: cultivar Columbia

C:Genetics:

A:Map position: 1

A:Note: ZCF61

Query Match 12.6%; Score 230.5; DB 2; Length 237;
Best Local Similarity 29.9%; Pred. No. 4.6e-10;
Matches 75; Conservative 46; Mismatches 89; Indels 41; Gaps 15;

QY	121	TNTVPFDIVPHEDGVDAVRVLPKIDSVLDGL-----ETVYEKHPISIQSFTDVIGHYIS	175
DB	5	TKREVPMVL---DDGTG---RVNVDSQGLGIALTVGSDFEKAEP-VSLVQALG-YLK	56
QY	176	GERPKGIQETEMKLVGATLVGVEGLVDN-NSVRLQPPKQGMQYLLSSQDPDSLQROE	234
DB	57	GKILGVHVRVVERVPIGLPLTVGGAARDGKGNVARIQREDOQ-PRVYVYIPIPDQLISKIG	115
QY	235	SSVRLMKVIAL---VEGFATCA--TLFPILRK--OYLROER-LRLKQMEEFQHEAQL	286
DB	116	DISRRFKTASMGVLTGLVILSKRYIEIKRIETLRRRRQFLKRVVD-----AA	168
QY	287	ISRAKP-----EDRESIKACVVCSSFKSCVFLBEGHVCSCTECYRALPEPKKPCIC	339
DB	179	ARRAKPVVGGGSRGDR-PDLCAVCLDQKNTAVAVECGHMCCTPCLQLT---RTCLPC	224
QY	340	ROATRVVPLV 350	
DB	225	RERIQOVAKIXY 235	

RESULT 2

P96582 hypothetical protein P1511.25 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: P96582

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B96582
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-383 <STO>
 A:Cross-references: UNIPROT:Q9SVH3; UNIPARC:UPI00000A0245; GB:AEO05173; NID:g4587558; PI
 A:Genetics:
 A:Gene: F1511.25
 A:Map position: 1

Query Match 11.0%; Score 201; DB 2; Length 383;
 Best Local Similarity 21.5%; Pred. No. 1.4e-07;
 Matches 81; Conservative 71; Mismatches 171; Indels 54; Gaps 13;
 14 ILGTTVTALYV-YRQKARVQELKAKVHLGDLKSLSEAPGKCP-----64
 23 ILGLTAVSAGSALKYASTNALKTKDAPEVSI-SDLRSLPASHDKSETDNRKSD 81
 65 --YVIEGAVSVKETINSQFENCKGVIQRLTQEHKMNNTTHLMNCSKIIH--120
 82 QRIVVAGVVK--FKISGDEGVKNNVILSPETGDKLIIQRTQTVYSQMKLPSTGH 139
 121 -----TNTPEPDLVPHEDGV--VAVRV--LKPLDSVDLGLGYEYERK 159
 140 RFMLERSLRKHGAFTRTVPVIVGKQDSNSFVAVMNGSQPLP-----LTTYVNL 194
 160 HPSIQSFVDVIGHYISERPKGIOETEMLKVATLTGVELVDNNSVFLQPKQMQY 219
 195 QPINSSTLQA--FLYPDYVGLDIEKILPFGDITAVG-IYSPNNGVEIKSCODLPY 250
 220 YLSSQDPSLQROESSVRLMKVLAIVGFATCATLFFILRKQYLRQERLRKQOEER 279
 251 FLSEMTDKMKIEMEGTNPFLIGSVILGIVSGILSYAVRW---NKKMKMHOREI 306
 280 QEHNAQLSRAPKPDRESLSKA--CVVCLSSFKSCVFLGCHVCSCTEYRALPEP--KK 335
 307 PQRNDVSVDEPDADIEPDGELCVICVSRVRVPAFIPGHVAVCRRCASVTERELNPK 366
 336 CPICRQATRVIPLYNS 352
 367 CPVCLQSIKSGMKVYIS 383

RESULT 3
 B96664
 Probable RING zinc finger protein T12P18.8 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: B96664
 R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B96664
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-115 <STO>

A:Cross-references: UNIPROT:Q9CAK3; UNIPARC:UPI00000A29C7; GB:AEO05173; NID:g6358794; P
 C:Species: *Homo sapiens* (man)
 A:Gene: T12P18.8
 A:Map position: 1

Query Match 7.6%; Score 138.5; DB 2; Length 115;
 Best Local Similarity 30.2%; Pred. No. 0.0015;
 Matches 35; Conservative 18; Mismatches 46; Indels 17; Gaps 4;
 248 GPATCATLFFILR--KOYLQROERLRKQOEERQEHNAQLSRAPKPDRESLSKA---301
 2 GF-TVLGVFLITKTHVIDSVLERRRRQLQKVLDAAKRAELSESGNSGNTRESISDSTXK 60
 302 -----CVVCLSSFKSCVFLGCHVCSCTEYRALPEPKKCPICRQATRVIPLY 350
 61 EDAPVDLCVLCLEQENAVFVPCGMCCCTACSSHL---TSCPLCRRIIDILAVKTY 113

RESULT 4
 S68450
 Apoptosis inhibitor hiap-2 - human
 C:Species: *Homo sapiens* (man)
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: S68450
 R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani,
 A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP
 A:Reference number: A58182; MUID:96149249; PMID:8552191
 A:Accession: S68450
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-618 <LIS>
 A:Cross-references: UNIPROT:Q13490; UNIPARC:UPI00000A435C; EMBL:U45879; NID:g1184317; PI
 A:Function: apoptosis suppressor
 A:Keywords: apoptosis; zinc finger
 C:Keywords: apoptosis; zinc finger
 F:567-611/Domain: RING zinc finger homology <RNG>

Query Match 7.6%; Score 138.5; DB 2; Length 618;
 Best Local Similarity 21.5%; Pred. No. 0.014;
 Matches 67; Conservative 50; Mismatches 119; Indels 75; Gaps 13;
 82 QFVENCKVIOQLTQEHKMNNTTHLMNCSKIIHRTVTPFDLPVHEDGVDAVRV 141
 343 EFVDEIQGRYHLL--EQLLSTDTTGENADPPIH-----FGGSSSDAVMM 391
 142 LKPL--DSVDLGL-----ETVYEKFPSPISF--TDVIGHYISGERPKGIOE---TE 186
 392 NTPVVKSLALEMGFNRDLVKQTVLSKILTTGENYKTVNDIVSALINAEDEKEKEKQAE 451
 187 EMLKVGATLTGVGEL-----VLDN-----NSVRLQPP--KQMQVYLSQD-FD 227
 452 EMASDLSLIRKNRAALFQQLTCVLPILIDNLKANVINKQHDIIKQTKQIPLOARELID 511
 228 SLQROESSVRLMKVLAIVGFATCATLFFILRKQYLRQERLRKQOEER 511
 512 TIWVGNAAAMIPKCKLEIDSTLYKLFVDMKMKYIPTEBVSGLSLEQARRQOE---568
 282 HEAQLLSRAKEDRESLSKACVVCVLSFKSCVFLGCHVCSCTEYRALPEPKKCPICRQ 341
 569 -----RTCKVCMDEKVSVVFIPCGHLVVCQBC--APSLRKCPICRG 607
 342 AITRVIPLYNS 352
 608 IIKGVTRFLS 618

RESULT 5
 S68449
 Apoptosis inhibitor hiap-1 - human
 C:Species: *Homo sapiens* (man)
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: S68449

280 -----QEHEAQLSPRAKPEDRESLSACVWCLSSFKSCVFLECGHVCSTECYPALPE 332

C: Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 6.7%; Score 123; DB 2; Length 275;

Best Local Similarity 22.8%; Pred. No. 0.07;
Matches 44; Conservative 30; Mismatches 55; Indels 64; Gaps 9;

QY 183 QSTEMKATGATLTGCVGLVLDNNSVRLPPKQMOYIIS--QPDFSLROESSVRLM 240

DB 124 QPEQWADGFPYTG---DNTKC-----FYCDGGIKDMEPDVMEQHR-W 168

QY 241 KVLALVFGATCATLFFILRKQYLR-----OERLRLKMOQEEF 279

DB 169 -----PDRCAVYVLVGRDYVQVITBEACVLPGEENTVSTAFAVSEPIPETKLESP 220

QY 280 QEHQAQLSRAPDEDESLKSACVVCISSEKSCVPLECGHVCSTECYRALPEPKKCPIC 339

DB 221 QVEDSLTCKICVYEE-----CIYC-----FPGGHVAVCAKCALSV---DKCPMC 262

QY 340 QQAIRVIVLINS 352

DB 263 RKIVTSVLKVPFS 275

RESULT 12

T01251
hypothetical protein Ac2g38190 [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein Fl6M14.12

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

R:Roundley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1998

A:Description: Arabidopsis thaliana chromosome II BAC Fl6M14 genomic sequence.

A:Reference number: Z14213

A:Accession: T01251

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-124 <ROU>

A:Cross-references: UNIPROT:O80444; UNIPARC:UPI00000A85FB; EMBL:AC003028; NID:g3335356;

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84802

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-124 <STO>

A:Cross-references: UNIPARC:UPI00000A85FB; GB:AE002093; NID:g3335367; PIDN:AAC27168.1; C

C:Genetics:

A:Gene: At2g38190; Fl6M14.12

A:Map position: 2

A:Introns: 100/2

Query Match 6.6%; Score 121.5; DB 2; Length 124;
Best Local Similarity 32.0%; Pred. No. 0.032;
Matches 24; Conservative 13; Mismatches 29; Indels 9; Gaps 2;

QY 277 EEFQHEAQLSRAPDEDESLKSACVVCISSEKSCVPLECGHVCSTECYRALPEPK-K 335

DB 56 EEFMGNDGASNR-----RRLCAICFDVPRDCFLPCGHVSVCYCGTTMGADDS 107

QY 336 CPTCQATRVIVLY 350

DB 108 CPTCRKMKKVKRY 122

RESULT 13

D36828
OR13 protein - Autographa californica nuclear polyhedrosis virus

C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: D36828; C72853

R:Brannagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.

Virology 191, 1003-1008, 1992

A:Title: Sequence, genomic organization of the EcoRI-A fragment of Autographa californica VP8 of rotavirus.

A:Reference number: A44221; MUID:93079853; PMID:1333113

A:Accession: D36828

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-286 <BRA>

A:Cross-references: UNIPROT:P41435; UNIPARC:UPI0000178P99; GB:S52569

R:Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.

Virology 202, 586-605, 1994

A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.

A:Reference number: A72850; MUID:94303173; PMID:8030224

A:Accession: C72853

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-199, 'L', 201-286 <AVR>

A:Cross-references: UNIPARC:UPI000012D0B8; GB:L22858; NID:9510708; PIDN:AAA6657.1; PID:

C:Genetics:

A:Gene: Ac-IAP1

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 6.4%; Score 118; DB 2; Length 286;
Best Local Similarity 40.4%; Pred. No. 0.18;
Matches 21; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

QY 299 KSACVCLSSFFKSCVPLECGHVCSTECYRALPEPKKCPICQATRVIVLY 350

DB 235 KYECVCLERQDAVLMPCRHFCVVCQCYFGIDQ--KCPTCRQDVTDFIKIF 284

RESULT 14

T41772

IAP1 orf27 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C:Species: Bombyx mori nuclear polyhedrosis virus, BmSNV

A:Variety: isolate T3

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T41772

R:Gomi, S.; Majima, K.; Maeda, S.

J. Gen. Virol. 80, 1323-1337, 1999

A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.

A:Reference number: Z22020; MUID:99281911; PMID:10355780

A:Accession: T41772

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-292 <KAN>

A:Cross-references: UNIPROT:O92394; UNIPARC:UPI00000F314F; EMBL:L33180; NID:g3745835; PI

A:Experimental source: isolate T3

C:Genetics:

A>Note: iap1

C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 6.4%; Score 118; DB 2; Length 292;
Best Local Similarity 40.4%; Pred. No. 0.18;
Matches 21; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

QY 299 KSACVCLSSFFKSCVPLECGHVCSTECYRALPEPKKCPICQATRVIVLY 350

DB 241 KYECVCLERQDAVLMPCRHFCVVCQCYFGIDQ--KCPTCRQDVTDFIKIF 290

RESULT 15

T16028

hypothetical protein F10D7.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Aug-2002

C:Accession: T16028

R:Raich, A.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F10D7.

A:Reference number: Z18448

A:Accession: T16028

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-824 <TAI>
A:Cross-references: UNIPARC:UPI00001797E7; EMBL:U40945; NID:G1072208; PID:G1072213; PIDN
C:Gene: CESP:PI007.5
A:Introns: 83/1; 108/1; 136/2; 174/1; 217/1; 236/2; 278/2; 325/3; 354/3; 384/1; 399/3; 4
C:Superfamily: fruit fly finger protein neutralized; RING finger homology
F:769-817/Domain: RING finger homology <RRN>

Query Match 6.4%; Score 117.5; DB 2; Length 824;
Best Local Similarity 34.7%; Pred. No. 0.77;
Matches 26; Conservative 7; Mismatches 35; Indels 7; Gaps 2;

QY	279	FOEHQAQLSRKPEDRESLSKACVVCISFHSKCVFLECGHVCSCTECVRALPEPK-KCP	337
Db	756	FORNEGGAQGVNKGDE-----CTTCMDAPVNSVLYTCGHMCWCFECGRLLTTKGTCP	809
QY	338	ICRQAITRVIPLYNS	352
Db	810	ICRAPVODVIKTKYS	824

Search completed: February 24, 2006, 08:30:08
Job time : 43 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 24, 2006, 08:22:04 ; Search time 188 Seconds
(without alignments)
822.667 Million cell updates/sec

Title: US-09-978-360A-437

Perfect score: 1831
Sequence: 1 MESGRPSLQFILGTSV.....PKKPCICQATRVIPLYNS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: A_Geneseq.21.*
- 2: geneeqp1990s.*
- 3: geneeqp2000s.*
- 4: geneeqp2001s.*
- 5: geneeqp2002s.*
- 6: geneeqp2003as.*
- 7: geneeqp2003bs.*
- 8: geneeqp2004s.*
- 9: geneeqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1831	100.0	352	3	AA825794 Human sec
2	1831	100.0	352	4	AAE06602 Human pro
3	1831	100.0	352	4	ABB50174 Human tra
4	1831	100.0	352	4	AB75380 Human sec
5	1831	100.0	352	5	ABP61461 Human NF-
6	1831	100.0	352	5	ABP61461 Human NF-
7	1831	100.0	352	8	ADP19181 Human sec
8	1831	100.0	352	8	ADR89550 Apoptosis
9	1826	99.7	392	6	AAU15848 Human nov
10	1826	99.7	392	6	ABUS4917 Human nov
11	1824	99.6	352	5	ABP61460 Human pro
12	1818	99.3	352	4	AA894353 Human pro
13	1795	98.0	511	8	ADU02286 Novel hum
14	1328.5	72.6	263	6	ABJ38658 Human nuc
15	901	49.2	174	4	AAU16309 Human nov
16	901	49.2	174	6	ABUS5378 Human nov
17	854	46.6	165	5	ABR90304 Human pol
18	445	24.3	91	2	AAV13137 Human sec
19	442.5	24.2	338	4	AB857873 Drosophil
20	439	24.0	90	2	AAV11645 Human 5'
21	437	23.9	88	2	AAV11871 Human 5'
22	267.5	14.6	338	8	ADT56108 Human pol
23	252.5	13.8	375	8	ADT60537 Plant pol
24	231	12.6	232	8	ADX78340 Plant ful

25	201	11.0	383	3	AAG32339
26	200	10.9	389	3	AAG10096
27	200	10.9	393	3	AAG10095
28	188.5	10.3	332	7	ADD25209
29	188.5	10.3	332	8	ADN61224
30	187.5	10.2	342	3	AAG32340
31	186.5	10.2	242	3	AAG10097
32	184.5	10.1	163	8	ADY09490
33	183	10.0	235	8	ADX67603
34	177	9.7	206	3	AAG32341
35	172	9.4	366	8	ADT57025
36	163	8.9	257	4	AAE10909
37	163	8.9	372	3	AAV56882
38	163	8.9	403	7	ABM85233
39	155.5	8.5	234	6	ADY52508
40	155.5	8.5	303	6	ADA54907
41	155.5	8.5	696	6	ADA54857
42	155.5	8.5	723	5	AAV96308
43	155.5	8.5	723	5	ABG32886
44	155.5	8.5	723	7	ADB64418
45	155.5	8.5	723	9	ADY52503

ALIGNMENTS

RESULT 1	AA825794	standard; protein, 352 AA.
ID	AA825794	
AC	AA825794;	
DT	28-NOV-2000	(first entry)
XX		
DE	Human secreted protein SEQ ID #106.	
XX		
KW	Human; secreted protein; forensic procedure; gene therapy;	
KW	chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;	
KW	cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;	
KW	brain disorder; skeletal muscle disorder; eye disorder; obesity;	
KW	mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease;	
KW	neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;	
KW	septic shock; impotence.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200037491-A2.	
XX		
PD	29-JUN-2000.	
XX		
PF	20-DEC-1999;	99WO-IB002058.
XX		
PR	22-DEC-1998;	98US-0113686P.
XX		
PR	25-JUN-1999;	99US-0141032P.
XX		
PA	(GSEST) GENSET.	
XX		
PI	Bougueleret L, Dumas J, Duclert A;	
XX		
DR	WPI: 2000-442637/38.	
XX		
DR	N-PSDB; AAA87756.	
XX		
PT	Polynucleotides and polypeptides encoding proteins with signal peptides,	
XX	useful in diagnostic, forensic, gene therapy and chromosome mapping	
XX	procedures.	
PS	Claim 9; Page 279-280; 306pp; English.	
XX		
CC	This sequence represents a human secreted protein amino acid sequence.	
XX		
CC	The invention relates to sequences AA87725-AA8774 which encode human	
XX	secreted proteins AA825763-B25812. The proteins include signal peptides.	
XX	included in the invention are a host cell containing one of the cDNA	
XX	sequences, and a purified antibody capable of binding to one of the	

secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the cDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondrial cytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, dementia, hyperlipidaemia, septic shock and impotence.

Sequence 352 AA;

Query Match 100.0%; Score 1831; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.4e-168;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSGRPSLCOFILGTTSTVTAALYSYRQKARVSOELGAKKXVHIGEDIKSILSEAPG 60
DB 1 MESSGRPSLCOFILGTTSTVTAALYSYRQKARVSOELGAKKXVHIGEDIKSILSEAPG 60
QY 61 KCVPAVIEGAVRSVKETLNSQFVENCXGVIORLTLOEHKVMNRTHLWDCSKIIHOR 120
DB 61 KCVPAVIEGAVRSVKETLNSQFVENCXGVIORLTLOEHKVMNRTHLWDCSKIIHOR 120
QY 121 TNNVFPDLVPHEDGDVAVRVLKPLDSVDGLFTVEYKFPHSIQSFVDVIGHYISGERPK 180
DB 121 TNNVFPDLVPHEDGDVAVRVLKPLDSVDGLFTVEYKFPHSIQSFVDVIGHYISGERPK 180
QY 181 GIOETHEMLKVGATLTGVELVLDNNSVRLQPPKQGYLYSSODPSSLQRESSVRLW 240
DB 181 GIOETHEMLKVGATLTGVELVLDNNSVRLQPPKQGYLYSSODPSSLQRESSVRLW 240
QY 241 KVLALVGFATCATLFFILRKQYLOEROERLTKOMOEFOHEBAQLLSRAKPEDRESLKS 300
DB 241 KVLALVGFATCATLFFILRKQYLOEROERLTKOMOEFOHEBAQLLSRAKPEDRESLKS 300
QY 301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKPCICQATIRVILPLVNS 352
DB 301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKPCICQATIRVILPLVNS 352

RESULT 2

ID AAE06602 standard; protein; 352 AA.

AC AAE06602;

XX 25-SEP-2001 (first entry)

XX Human protein having hydrophobic domain, HP10649.

XX Human; hydrophobic domain; gene therapy; nutritional supplement;
XX cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;
XX multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
XX haemotopoiesis; tissue growth activity; Parkinson's disease; cytostatic;
XX Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;
XX haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
XX contraceptive; antinflammatory; antiinflammatory.

OS Homo sapiens.

XX MO200149728-A2.

XX 12-JUL-2001.

PD 28-DEC-2000; 2000MO-JP009359.

XX 06-JAN-2000; 2000JP-00000585.

PR 06-JAN-2000; 2000JP-00000588.
PR 11-JAN-2000; 2000JP-00002299.
PR 03-FEB-2000; 2000JP-00026862.
PR 03-MAR-2000; 2000JP-00058367.

XX (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.

PI Kato S, Kimura T;

DR WPI; 2001-418355/44.

DR N-PSDB; AAD12597.

PT Human proteins with hydrophobic domains and the nucleic acids encoding
PT them, useful for preventing diagnosing and treating e.g. cancer,
PT Alzheimer's and inflammation.

XX Claim 1, Page 122; 563pp; English.

XX The present sequence is human protein with hydrophobic domain, HP10649.
CC The polynucleotide and polypeptide of the invention may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate polypeptide expression. The polynucleotides may be used to
CC produce the polypeptide, by inserting the nucleic acids into a host cell
CC and culturing the cell to express the protein. The polynucleotides and
CC its complementary sequences may also be used as DNA probes in diagnostic
CC assays and also used in gene therapy. The polypeptides may also be used
CC as antigens in the production of antibodies and in assays to identify
CC modulators of polypeptide expression and activity. The polypeptides and
CC nucleic acids may be used as nutritional supplements, to modulate
CC cytokine and cell proliferation activity, to modulate immune stimulation
CC or suppression (e.g. for the treatment of microbial infections and
CC autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and
CC insulin-dependent diabetes), to modulate haematopoiesis, to modulate
CC tissue growth activity (e.g. for the treatment of Parkinson's disease,
CC Huntington's disease and Alzheimer's disease), to modulate actinin and
CC inhibin activity (e.g. for controlling fertility), to modulate
CC chemotactic and chemokinetic activity, to modulate haemostatic and
CC thrombolytic activity, to modulate receptor ligand activity, to modulate
CC inflammation and to inhibit tumour growth

XX Sequence 352 AA;

Query Match 100.0%; Score 1831; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.4e-168;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSGRPSLCOFILGTTSTVTAALYSYRQKARVSOELGAKKXVHIGEDIKSILSEAPG 60

DB 1 MESSGRPSLCOFILGTTSTVTAALYSYRQKARVSOELGAKKXVHIGEDIKSILSEAPG 60

QY 61 KCVPAVIEGAVRSVKETLNSQFVENCXGVIORLTLOEHKVMNRTHLWDCSKIIHOR 120

DB 61 KCVPAVIEGAVRSVKETLNSQFVENCXGVIORLTLOEHKVMNRTHLWDCSKIIHOR 120

QY 121 TNNVFPDLVPHEDGDVAVRVLKPLDSVDGLFTVEYKFPHSIQSFVDVIGHYISGERPK 180

DB 121 TNNVFPDLVPHEDGDVAVRVLKPLDSVDGLFTVEYKFPHSIQSFVDVIGHYISGERPK 180

QY 181 GIOETHEMLKVGATLTGVELVLDNNSVRLQPPKQGYLYSSODPSSLQRESSVRLW 240

DB 181 GIOETHEMLKVGATLTGVELVLDNNSVRLQPPKQGYLYSSODPSSLQRESSVRLW 240

QY 241 KVLALVGFATCATLFFILRKQYLOEROERLTKOMOEFOHEBAQLLSRAKPEDRESLKS 300

DB 241 KVLALVGFATCATLFFILRKQYLOEROERLTKOMOEFOHEBAQLLSRAKPEDRESLKS 300

QY 301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKPCICQATIRVILPLVNS 352

DB 301 ACVCLSSFKSCVFLGCGHVCSTECYRALPEPKKPCICQATIRVILPLVNS 352

RESULT 3

ID	ABB50174	standard; protein; 352 AA.
XX	ABB50174;	
AC	ABB50174;	
XX		
DT	05-FEB-2002	(first entry)
XX		
DE	Human transcription factor TRFX-25.	
XX		
KM	Human; transcription factor; TRFX; cell proliferative disease;	
KW	autoimmune disease; inflammatory; neurological disease;	
RN	developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV;	
XX	neuroprotective; antiinflammatory; gene therapy.	
OS	Homo sapiens.	
XX		
PN	MO200127277-A2.	
PD		
PF	04-OCT-2001.	
PR	13-MAR-2001; 2001WO-US008117.	
PA	13-MAR-2000; 2000US-018986P.	
PI	(INCY-) INCYTE GENOMICS INC.	
PJ	Hillman JT, Baughn MR, Yue H, Lal P, Lu DM, Patterson C, J;	
PI	Azizmai Y, Bandman O, Tang YT, Matchur P, Shah P, Au-Young J;	
PI	Reddy R;	
XX	WPI: 2001-570896/64.	
DR	N-PSDB; ABA82398.	
PT	Novel transcription factor polypeptides, used to treat diseases	
PT	associated with altered activity and expression of TRFX, and to screen	
PT	for agents capable of modulating its activity.	
XS		
XX	Claim 1; Page 168-169; 327pp; English.	
XX		
CC	The present sequence is the protein sequence for a human transcription	
CC	factor. The transcription factor and its coding sequence are useful in	
CC	the diagnosis, treatment and prevention of diseases associated with	
CC	altered expression of the transcription factor e.g. cell proliferative,	
CC	autoimmune/inflammatory, neurological and developmental disorders. A	
CC	number of specific disorders/diseases are given in the specification,	
CC	including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS,	
CC	allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic	
CC	dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout,	
CC	Graefe's disease, multiple sclerosis, osteoarthritis, pancreatitis,	
CC	polioidis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative	
CC	colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's	
CC	disease, stroke, and viral, bacterial, fungal and protozoal infections	
XX		
SQ	Sequence 352 AA;	
Query Match	100.0%; Score 1831; DB 4; Length 352;	
Best Local Similarity	100.0%; Pred. No. 1.4e-166;	
Matches 352; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
Dy	1 MESGGRPSLCOFILILGTTSVTAALSYVRKARVSOLKAKKYHLGEDLSIIEAAG 60	
Dd	1 MESGGRPSLCOFILILGTTSVTAALSYVRKARVSOLKAKKYHLGEDLSIIEAAG 60	
Dy	61 KCVPAVVEGA VRSAKETINSOFENCKGVIRLTLOEHKWMMNRTHLMNDCKIIHOR 120	
Dd	61 KCVPAVVEGA VRSAKETINSOFENCKGVIRLTLOEHKWMMNRTHLMNDCKIIHOR 120	
Dy	121 TNNVPFDLPVPHEDGDVA VRVLKPLDSVDLGLETYYEKHPISIQSFTDVIYHYSIGERPK 180	
Dd	121 TNNVPFDLPVPHEDGDVA VRVLKPLDSVDLGLETYYEKHPISIQSFTDVIYHYSIGERPK 180	
Dy	181 GIQREHEMLTKGATITTCGELAVLDNNNSVRLQPPKGGMQYLLSSODFSLIQOESSVRLW 240	
Dd	181 GIQREHEMLTKGATITTCGELAVLDNNNSVRLQPPKGGMQYLLSSODFSLIQOESSVRLW 240	

Dd		181	GJOETEMMLKVGATLTGVELLDNNNSVRLQPPKQGMYILSSQDFPSLLQROESSVRLM	24
Oy		241	KYLALVFGPATCATLFFILRKQYIQRORRLALKMOSEFQEHAKQLISRAKPEDRESLK	300
Dd		241	KVLALVFGPATCATLFFILRKQYIQORERLTKMOSEFOHEAKQLISRAKPEDRESLK	300
Oy		301	ACVCCLSSFKSCVFLECGHVSCTECYALPEPKPCICRQALTRVPLVNS	352
Dd		301	ACVCCLSSFKSCVFLECGHVSCTECYALPEPKPCI CRQALTRVPLVNS	352
	RESULT 4			
	AAB75380			
XX	ID	AAB75380	standard; protein; 352 AA.	
XX	AA	AAB75380;		
XX	AC			
XX	DT	05-APR-2001	(first entry)	
XX	DE			
XX	Human		secreted protein #39.	
XX	Secreted		protein; prevention; treatment; diagnosis; disease; infection.	
XX	Homo sapiens.			
XX	NO200100806-A2.			
XX	EN			
XX	PD	04-JAN-2001.		
XX	PF	21-JUN-2000;	2000MO-IB000951.	
XX	PR	25-JUN-1999;	99US-0141032P.	
XX	PR	21-DEC-1999;	99US-00469099.	
XX	PA	(BEST)	GENSET.	
XX	PI	Dumas Milne Edwards J,	Bougueleret L, Jobert S;	
XX	DR	WPI; 2001-071487/08.		
XX	PT	49 Secreted proteins and the nucleic acids encoding them, useful in gene therapy and for detecting similar sequences in samples.		
XX	PS	Claim 10; Page 299-300; 307bp; English.		
XX	CC	The present invention relates to 49 secreted proteins and the cDNAs encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression		
XX	CC			
XX	Sequence	352 AA;		
XX	SQ			
Oy	Query Match	100.0%;	Score 1831; DB 4; Length 352;	
Oy	Best Local Similarity	100.0%;	Pred. No. 1,4e-168;	
Oy	Matches 352;	Conservative 0;	Mismatches 0; Gaps 0	
Dd		1	MESGGRPSPCOFILIGTTSVVTALYSYVRQKARVSOELKGAKKVHLGEDLSILSBAG	60
Dd		1	MESGGRPSPCOFILIGTTSVVTALYSYVRQKARVSOELKGAKKVHLGEDLSILSBAG	60
Oy		61	KCPYAVIVTGAVRSVKETLSNQFVENCNGVQRLTLQEHKKVMNRTHLMNDSKIHOR	120
Dd		61	KCPYAVIVTGAVRSVKETLSNQFVENCNGVQRLTLQEHKKVMNRTHLMNDSKIHOR	120
Oy		121	TNTVPDPDLPHBEDGVDAVRVLKPLDSDVDLGLFTVYEKFPSIQSFTDVIGHYISGERPK	180
Dd		121	TNTVPDPDLPHBEDGVDAVRVLKPLDSDVDLGLFTVYEKFPSIQSFTDVIGHYISGERPK	180
Oy		181	GJOETEMMLKVGATLTGVELLDNNNSVRLQPPKQGMYILSSQDFPSLLQROESSVRLM	240
Dd		181	GJOETEMMLKVGATLTGVELLDNNNSVRLQPPKQGMYILSSQDFPSLLQROESSVRLM	240
Oy		241	KVLALVFGPATCATLFFILRKQYIQORERLTKMOSEFOHEAKQLISRAKPEDRESLK	300
Dd		241	KVLALVFGPATCATLFFILRKQYIQORERLTKMOSEFOHEAKQLISRAKPEDRESLK	300

Db 241 KYIALVGFATCATLFFILRKQYLQROERLRKQMOEFQHEAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKPCPICRAITRVIPLYNS 352
 Db 301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKPCPICRAITRVIPLYNS 352

RESULT 5

ABP61461
 ID ABP61461 standard; protein; 352 AA.

AC ABP61461;

DT 30-SEP-2002 (first entry)

DE Human NF-kB activating protein SEQ ID NO 75.

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
 KW immunomodulator; cytosolic; antiinfective; osteopathic; noctropic;
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

OS Homo sapiens.

PN WO200253737-A1.

PD 11-JUN-2002.

PF 25-DEC-2001; 2001WO-JP011389.

PR 28-DEC-2000; 2000JP-00402288.

PR 26-MAR-2001; 2001JP-00088912.

PR 24-AUG-2001; 2001JP-00254018.

XX (ASAH) ASAH KASEI KOGYO KK.

PI Matsuda A, Honda G, Muramatsu S, Nagano Y;

DR WPI; 2002-583617/62.

XX N-PSDB; ABQ91949.

PT NF-approximatelykB activating gene and expressed protein, applicable in
 PT diagnosis and screening inhibitors or promoters to control excessive
 PT activation or inhibition for treating e.g. inflammations, autoimmune
 PT diseases and cancer.

PS Claim 1; Page 349-352; 841pp; Japanese.

XX The invention relates to a purified protein (I), comprising one of 90
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
 CC the sequences but with some amino acids deleted, substituted or added and
 CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
 CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
 CC inhibitors or promoters to control excessive activation or inhibition and
 CC for treating e.g. inflammations, autoimmune diseases, cancers,
 CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
 CC disorders

XX Sequence 352 AA;

QY Query Match 100.0%; Score 1831; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.4e-168;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGGRPSLCQFILGTTSVVTAALYSVYRQKARVSQELKGAKKVLGEDIKSLISEAPG 60

Db 1 MESGGRPSLCQFILGTTSVVTAALYSVYRQKARVSQELKGAKKVLGEDIKSLISEAPG 60

QY 61 KCVPAVAVIGAVSVKELINSQFVENCCKGVICQLTLOEHKMWNRTHLMNDSKIIHOR 120

Db 61 KCVPAVAVIGAVSVKELINSQFVENCCKGVICQLTLOEHKMWNRTHLMNDSKIIHOR 120

QY 121 TWTPFDLVPHEBDGDVAVRVLKPLDSVDLGLFTYKFKHPSIQSFPTDIGHYIGGERPK 180
 Db 121 TWTPFDLVPHEBDGDVAVRVLKPLDSVDLGLFTYKFKHPSIQSFPTDIGHYIGGERPK 180
 QY 181 GIQTEEMKAVGATLTGVEGLVDNNNSVRLQPKQMGQYILSSQDPDSLQOESSVRLM 240
 Db 181 GIQTEEMKAVGATLTGVEGLVDNNNSVRLQPKQMGQYILSSQDPDSLQOESSVRLM 240
 QY 241 KYIALVGFATCATLFFILRKQYLQROERLRKQMOEFQHEAQLLSRAKPEDRESLKS 300
 Db 241 KYIALVGFATCATLFFILRKQYLQROERLRKQMOEFQHEAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKPCPICRAITRVIPLYNS 352
 Db 301 ACVCLSSFKSCVFLFCGHVCSCTECYRALPEPKPCPICRAITRVIPLYNS 352

RESULT 6

ABB97404
 ID ABB97404 standard; protein; 352 AA.

AC ABB97404;

DT 27-JUN-2002 (first entry)

DE Novel human protein SEQ ID NO: 672.

XX Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
 KW antiinfectivity; cerebroprotective; cytosolic; rheumatic; gene therapy;
 KW neuroprotective; antiparkinsonian; protein therapy; EST;
 KW expressed sequence tag.

OS Homo sapiens.

PN WO200222660-A2.

PD 21-MAR-2002.

PF 10-SEP-2001; 2001WO-US026015.

PR 11-SEP-2000; 2000US-00659671.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;

DR WPI; 2002-292408/33.

XX N-PSDB; ABN32590.

PT An isolated polynucleotide for treating diseases associated with its
 PT encoded polypeptide such as cancer and multiple sclerosis.

PS Claim 20; SEQ ID NO 672; 509pp; English.

XX The present invention provides the protein and coding sequences of 444
 CC novel human proteins. These were isolated from expressed sequences tags
 CC (ESTs). They can be used to stimulate cell growth, to regulate
 CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
 CC e.g. in burn treatment, to regulate the immune system e.g. to treat
 CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
 CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
 CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
 CC rheumatoid arthritis, and to treat nervous system disorders e.g.
 CC Parkinson's disease. The present sequence is a protein of the invention

XX Sequence 352 AA;

QY Query Match 100.0%; Score 1831; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.4e-168;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESGGRPSLCQFILGTTSVVTAALYSVYRQKARVSQELKGAKKVLGEDIKSLISEAPG 60

```

Db      1 MESSGRPSLCOFTLLGTTSSVTALALYSYVRQKARVSQELKGAKVHLGEDLSILSEAPG 60
Qy      61 KCPYAVIEGAVRSVKETLNSQFVENCCKGVIRLTLQEHKVMWNRTHLMDCKSIHOR 120
Db      61 KCPYAVIEGAVRSVKETLNSQFVENCCKGVIRLTLQEHKVMWNRTHLMDCKSIHOR 120
Qy      121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLETVYEKEFHPSIOSFTDVIIGHYISGERPK 180
Db      121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLETVYEKEFHPSIOSFTDVIIGHYISGERPK 180
Qy      181 GIOETEMLKVGATLTGVGELVLDNNSVRLQPPKQGMQYLLSSODFSLQROESSVRLM 240
Db      181 GIOETEMLKVGATLTGVGELVLDNNSVRLQPPKQGMQYLLSSODFSLQROESSVRLM 240
Qy      241 KTLALVFGFATCATLFTFLRKQYLRQERLRLKQOEFOEHEAQLLSRAKPEDRESLKS 300
Db      241 KTLALVFGFATCATLFTFLRKQYLRQERLRLKQOEFOEHEAQLLSRAKPEDRESLKS 300
Qy      301 ACVVCLSFKSCVPLECGHVCSCTECYRALPEPKKPCICROAITRVIPLYNS 352
Db      301 ACVVCLSFKSCVPLECGHVCSCTECYRALPEPKKPCICROAITRVIPLYNS 352

RESULT 7
ADP19181
ID      ADP19181 standard; protein; 352 AA.
XX
AC      ADP19181;
XX
DT      26-AUG-2004 (first entry)
XX
DE      Human secreted polypeptide #32.
XX
KW      Human; secreted protein; genetic disease.
XX
OS      Homo sapiens.
XX
PN      US2004110939-A1.
XX
PD      10-JUN-2004.
XX
PF      15-OCT-2001; 2001US-00978360.
XX
PR      17-DEC-1998; 98WO-IB002122.
XX      09-FEB-1999; 99WO-IB000282.
XX      21-JUN-2000; 2000WO-IB000951.
XX      15-SEP-2000; 2000US-00663600.
XX
PA      (GSEST ) GENSET SA.
PI      Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C,
PI      Duclet A;
XX
DR      MPI: 2004-440404/41.
XX      N-PSDB; ADP18776.
XX
PT      New isolated polynucleotide encoding secreted polypeptide, useful for
PT      gene therapy, or in diagnostic procedures to identify individuals having
PT      genetic diseases resulting from abnormal expression of the genes.
XX
PS      Claim 2; SEQ ID NO 437; 113pp; English.
XX
CC      The invention relates to human cDNA sequences that encode human secreted
CC      proteins. The invention also relates to an antibody that specifically
CC      binds to a polypeptide of the invention and a method of binding the
CC      polypeptide to an antibody. The polynucleotides are useful for expressing
CC      the entire secreted proteins which they encode and for distinguishing
CC      human tissues and cells from non-human tissues and cells, and for
CC      distinguishing between human tissues and cells that do or do not express
CC      the polynucleotides comprising the cDNAs. The polynucleotides and
CC      polypeptides are useful in forensic procedures or diagnostic procedures
CC      to identify individuals with genetic diseases resulting from abnormal

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CC      expression of the genes corresponding to the cDNAs. The sequences are
CC      also useful in gene therapy to control or treat genetic diseases. This
CC      sequence represents a human secreted polypeptide of the invention. Note:
CC      The sequence data for this patent did not form part of the printed
CC      specification but was obtained in electronic format from USPTO at
CC      seqdata.uspto.gov/sequence.html.
XX
SQ      Sequence 352 AA;
XX
Query Match      100.0%; Score 1831; DB 8; Length 352;
Best Local Similarity 100.0%; Pred. No. 1,4e-168;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MESSGRPSLCOFTLLGTTSSVTALALYSYVRQKARVSQELKGAKVHLGEDLSILSEAPG 60
Db      1 MESSGRPSLCOFTLLGTTSSVTALALYSYVRQKARVSQELKGAKVHLGEDLSILSEAPG 60
Qy      61 KCPYAVIEGAVRSVKETLNSQFVENCCKGVIRLTLQEHKVMWNRTHLMDCKSIHOR 120
Db      61 KCPYAVIEGAVRSVKETLNSQFVENCCKGVIRLTLQEHKVMWNRTHLMDCKSIHOR 120
Qy      121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLETVYEKEFHPSIOSFTDVIIGHYISGERPK 180
Db      121 TMTVPFDLVPHEDGDVAVRVLKPLDSVDLGLETVYEKEFHPSIOSFTDVIIGHYISGERPK 180
Qy      181 GIOETEMLKVGATLTGVGELVLDNNSVRLQPPKQGMQYLLSSODFSLQROESSVRLM 240
Db      181 GIOETEMLKVGATLTGVGELVLDNNSVRLQPPKQGMQYLLSSODFSLQROESSVRLM 240
Qy      241 KTLALVFGFATCATLFTFLRKQYLRQERLRLKQOEFOEHEAQLLSRAKPEDRESLKS 300
Db      241 KTLALVFGFATCATLFTFLRKQYLRQERLRLKQOEFOEHEAQLLSRAKPEDRESLKS 300
Qy      301 ACVVCLSFKSCVPLECGHVCSCTECYRALPEPKKPCICROAITRVIPLYNS 352
Db      301 ACVVCLSFKSCVPLECGHVCSCTECYRALPEPKKPCICROAITRVIPLYNS 352

RESULT 8
ADR89550
ID      ADR89550 standard; protein; 352 AA.
XX
AC      ADR89550;
XX
DT      02-DEC-2004 (first entry)
XX
DE      Apoptosis-inducing protein, SEQ ID 74.
XX
KW      Cytostatic; Immunosuppressive; Neuroprotective; Vasotropic; Virucide;
KW      apoptosis; neurodegenerative disease; ischaemic disease; cancer;
KW      autoimmune disease; viral disease; human.
XX
OS      Homo sapiens.
XX
PN      WO2004078112-A2.
XX
PD      16-SEP-2004.
XX
PF      05-MAR-2004; 2004WO-JP002899.
XX
PR      07-MAR-2003; 2003JP-00061179.
XX      10-MAR-2003; 2003US-0452943P.
XX
PA      (ASAH-) ASAH KASEI PHARMA CORP.
PI      Muramatsu S, Takeda M, Matsuda A;
XX
DR      MPI: 2004-662343/64.
XX      N-PSDB; ADR89549.
XX
PT      New protein capable of inducing apoptosis, useful in screening for
PT      compounds that inhibit or induce apoptosis which may be used to treat
PT      neurodegenerative, ischemic, autoimmune and viral diseases, and cancer.

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XX Claim 1; SEQ ID NO 74; 316pp; English.

PS The present invention relates to novel purified proteins (i) and their
 CC coding sequences (ii) (ADRs9477-ADRs9550), which are capable of inducing
 CC apoptosis. The proteins (i) are useful as a target in screening for
 CC compounds that modulate apoptosis. Compounds that modulate the expression
 CC or activity of the protein may be useful in treating neurodegenerative
 CC diseases, ischemic diseases, cancer, autoimmune diseases, or viral
 CC diseases. Measurement of the expression or activity of the protein may
 CC also be used to diagnose or disease or a susceptibility to a disease.

XX Sequence 352 AA;

Query Match 100.0%; Score 1831; DB 8; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.4e-168;
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSGRPSLCOFILGTTSTVTALYSVYRQKARVSOELKGAKKHLGDLKSLSPAG 60
 Db 1 MESSGRPSLCOFILGTTSTVTALYSVYRQKARVSOELKGAKKHLGDLKSLSPAG 60
 QY 61 KCVYVAVTEGAVRSVKETLNSQFVENCCKVYQRLTQEHKVMWNRTHLWDCSKIIHQ 120
 Db 61 KCVYVAVTEGAVRSVKETLNSQFVENCCKVYQRLTQEHKVMWNRTHLWDCSKIIHQ 120
 QY 121 TNTVPFLDVPHEGDVAVRVLRKPLDSVDGLFTVYKFKHPSIOSFTDVGHTISGRPK 180
 Db 121 TNTVPFLDVPHEGDVAVRVLRKPLDSVDGLFTVYKFKHPSIOSFTDVGHTISGRPK 180
 QY 121 TNTVPFLDVPHEGDVAVRVLRKPLDSVDGLFTVYKFKHPSIOSFTDVGHTISGRPK 180
 Db 121 TNTVPFLDVPHEGDVAVRVLRKPLDSVDGLFTVYKFKHPSIOSFTDVGHTISGRPK 180
 QY 181 GIQTEEMLKVGATLTGVEGLVDNNSVRLQPPKQMGVYLISSQDFSLQROESSVRLM 240
 Db 181 GIQTEEMLKVGATLTGVEGLVDNNSVRLQPPKQMGVYLISSQDFSLQROESSVRLM 240
 QY 241 KVALVGFATNCATLFFILRKQYIQROBRRLIKMOSEFENHQAQLSRKPEDRSLS 300
 Db 241 KVALVGFATNCATLFFILRKQYIQROBRRLIKMOSEFENHQAQLSRKPEDRSLS 300
 QY 301 ACVVCLSSFFKSCVLECGHVCSTECYRALPEPKPCICQALTRVYPLVNS 352
 Db 301 ACVVCLSSFFKSCVLECGHVCSTECYRALPEPKPCICQALTRVYPLVNS 352

RESULT 9

ID AAV15848 standard; protein; 392 AA.

XX AC AAV15848;

DT 07-NOV-2001 (first entry)

XX Human novel secreted protein, Seq ID 801.

XX Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
 KW cardiact; vasotrophic; cerebroprotective; neurotropic; neuroprotective;
 KW antibacterial; virocidic; fungicidal; ophthalmological; vulnary;
 KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW cerebral ischaemia; angiogenesis; nervous system disorder;
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;
 KW wound healing; epithelial cell proliferation; skin aging; food additive;
 KW preservative; antiproliferative.

XX Homo sapiens.

XX MO200155322-A2.

XX 02-AUG-2001.

PF 17-JAN-2001; 2001MO-US001341.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-020515P.
 PR 07-JUN-2000; 2000US-0209667P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226682P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0233400P.
 PR 14-SEP-2000; 2000US-0233401P.
 PR 14-SEP-2000; 2000US-0233633P.
 PR 14-SEP-2000; 2000US-0233634P.
 PR 14-SEP-2000; 2000US-0233635P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234224P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235835P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI: 2001-488783/53.
DR N-PSDB: AAS25835.
XX
PT New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX

Query Match	99.7%;	Score 1826;	DB 4;	Length 392;
Best Local Similarity	99.7%;	Pred. NO. 5.1e-168;		
Matches 351; Conservative	1;	Indels	0;	Gaps 0
		Mismatches	1;	

RESULT 10
ABUS4917.
ID ABUS4917 standard; protein; 392 AA

DT	18-MAR-2003	(first entry)
XX		
DE		
XX	Human novel polypeptide #4.	
KM	Human; neural disorder; immune system disorder; renal disorder;	
KM	muscular disorder; respiratory disease; reproductive disorder;	
KM	gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;	
KM	hyperproliferative disorder; inflammatory disease; allergic reaction;	
KM	blood related disorder; cancer; immunosuppressive; antiinflammatory;	
KM	cardiovascular; nephrotoxic; cytostatic; antiallergic; thrombolytic;	
KM	haemostatic; antiarteriosclerotic.	

XX Homo sapiens.
 OS
 XX US200232753-A1.
 PN
 XX 19-SEP-2002.
 PD
 XX 17-JAN-2001; 2001US-00764864.
 PF
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 28-JUN-2000; 2000US-0214888P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 11-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 14-JUL-2000; 2000US-0217496P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 30-AUG-2000; 2000US-0228688P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236337P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251866P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX
 XX (ROSEN/) ROSEN C A.
 PA (RUBEN/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 XX WPI; 2003-147444/14.
 DR N-PSDB; ABX73176.
 XX
 PT New polypeptides and nucleic acids, useful in gene therapy for treating,
 PT inhibiting or preventing e.g. neural, immune system, muscular,
 PT respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
 PT renal disorders.

XX Claim 11; SEQ ID NO 801; 402bp; English.
 PS
 CC The invention relates to human novel polypeptides and their associated
 CC polynucleotides. The polypeptides and polynucleotides are useful in gene
 CC therapy for treating, inhibiting or preventing neural disorders, immune
 CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
 CC and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
 CC nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
 CC gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
 CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
 CC heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
 CC renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
 CC leukaemia), inflammatory diseases (e.g. septic shock, bursitis and
 CC appendicitis), allergic reactions and conditions (e.g. asthma), blood
 CC related disorders (e.g. thrombosis, atherosclerosis and myocardial
 CC infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and
 CC ABUS5748 represent human novel polypeptides of the invention
 XX
 SQ Sequence 392 AA;
 Query Match 99.7%; Score 1826; DB 6; Length 392;
 Best Local Similarity 99.7%; Pred. No. 5,1e-168;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSGGRPSLCQFILGTSVVTAAALYSYRQARVSOELKAKKHLGEDIKSLISEAPG 60
 DB 41 MSGGRPSLCQFILGTSVVTAAALYSYRQARVSOELKAKKHLGEDIKSLISEAPG 100
 QY 61 KCPYAVIAGAVRSYKETLNSQFVENCXGVIQRLTLOHKWVNNRTTHLMDSCXIIHQ 120
 DB 101 KCPYAVIAGAVRSYKETLNSQFVENCXGVIQRLTLOHKWVNNRTTHLMDSCXIIHQ 160
 QY 121 TMTVPEDLVPHEDGVAVRVKLPDSVDLGLFTYKEFHSISQFTTVIGHYISGERPK 180
 DB 161 TMTVPEDLVPHEDGVAVRVKLPDSVDLGLFTYKEFHSISQFTTVIGHYISGERPK 220
 QY 181 GIOETEMLKVGATLTGVEGLVDNNSVRLQPKQMGYYLSSQDFSLQROESSVRLW 240
 DB 221 GIOETEMLKVGATLTGVEGLVDNNSVRLQPKQMGYYLSSQDFSLQROESSVRLW 280
 QY 241 KYLALVFGPATCATLFTILRQYLOROERLRLKQOESEFOHEAQLSRAPEDRESLKS 300
 DB 281 KYLALVFGPATCATLFTILRQYLOROERLRLKQOESEFOHEAQLSRAPEDRESLKS 340
 QY 301 ACVCLSSFKSCVPLECGHVCSCTECYRALPEPKKCPICRAITRVIPLYNS 352
 DB 341 ACVCLSSFKSCVPLECGHVCSCTECYRALPEPKKCPICRAITRVIPLYNS 392
 RESULT 11
 ID ABP61460 standard; protein, 352 AA.
 AC ABP61460;
 XX
 DT 30-SEP-2002 (first entry)
 XX
 DE Human NF-KB activating protein SEQ ID NO 73.
 XX
 KW Human; NF-KB; nuclear factor kappa B; mouse; antiinflammatory;
 KW immunomodulator; cytostatic; antineoplastic; osteopathic; noctropic;
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200253737-A1.
 XX
 PD 11-JUL-2002.
 XX
 PF 25-DEC-2001; 2001WO-JP011389.

28-DEC-2000; 2000JP-00402288.
 PR 26-MAR-2001; 2001JP-00089912.
 PR 24-AUG-2001; 2001JP-00254018.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 PI Matsuda A, Honda G, Muramatsu S, Nagano Y;
 XX
 DR MPI: 2002-583617/62.
 DR N-PSDB; ABQ91948.
 XX
 PT NF-approximatelyB activating gene and expressed protein, applicable in
 PT diagnosis and screening inhibitors or promoters to control excessive
 PT activation or inhibition for treating e.g. inflammations, autoimmune
 PT diseases and cancer.
 PS Claim 1; Page 342-344; 841pp; Japanese.
 XX
 CC The invention relates to a purified protein (I), comprising one of 90
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
 CC the sequences but with some amino acids deleted, substituted or added and
 CC with a NF-κB (nuclear factor kappa B) activating effect. The protein and
 CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
 CC inhibitors or promoters to control excessive activation or inhibition and
 CC for treating e.g. inflammations, autoimmune diseases, cancers, and
 CC infections, bone diseases, AIDS, neurodegenerative diseases or ischemic
 CC disorders
 CC
 SQ Sequence 352 AA;
 XX
 Query Match 99.6%; Score 1824; DB 5; Length 352;
 Best Local Similarity 99.7%; Pred. No. 6 7e-169;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MESSGRPSLCQFILGTTSVTAALYSYVRKARVSOELKAKVHLGDLKSIISBAPG 60
 DB 1 MESSGRPSLCQFILGTTSVTAALYSYVRKARVSOELKAKVHLGDLKSIISBAPG 60
 QY 61 KCVPAVAVIEGAVRSVKEITNSQFVENCCKVIOQLTLOEHKVMWNRTHLMDCSKIIHOR 120
 DB 61 KCVPAVAVIEGAVRSVKEITNSQFVENCCKVIOQLTLOEHKVMWNRTHLMDCSKIIHOR 120
 QY 121 TMTVPFDLVPHEDGDVAVRVLPKPLDSVDLGLETVEYERKHPISQFTDVIIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGDVAVRVLPKPLDSVDLGLETVEYERKHPISQFTDVIIGHYISGERPK 180
 QY 181 GIQTEBMLKVGATLTGVELVDNNSVRLQPPKQGMQYISSLQPDSDLQOESSVRILM 240
 DB 181 GIQTEBMLKVGATLTGVELVDNNSVRLQPPKQGMQYISSLQPDSDLQOESSVRILM 240
 QY 241 KYLALVFGFATCATLFFILRKQYLOEROERLRLKQOEFOEHAQLLSRAKPEDRESLKS 300
 DB 241 KYLALVFGFATCATLFFILRKQYLOEROERLRLKQOEFOEHAQLLSRAKPEDRESLKS 300
 QY 301 ACVVCLSSFKSCVPLECGHVCSTECYRALPBPCKPICROAITRYIPYINS 352
 DB 301 ACVVCLSSFKSCVPLECGHVCSTECYRALPBPCKPICROAITRYIPYINS 352
 XX
 RESULT 12
 AAB94353
 ID AAB94353 standard; protein; 352 AA.
 XX
 AC AAB94353;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO:14873.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX
 OS Homo sapiens.
 XX

PM EP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 DR MPI: 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 PS Claim 8; SEQ ID NO 14873; 2537pp + Sequence Listing; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC oligonucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH1629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 CC
 SQ Sequence 352 AA;
 XX
 Query Match 99.3%; Score 1818; DB 4; Length 352;
 Best Local Similarity 99.7%; Pred. No. 2.6e-167;
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MESSGRPSLCQFILGTTSVTAALYSYVRKARVSOELKAKVHLGDLKSIISBAPG 60
 DB 1 MESSGRPSLCQFILGTTSVTAALYSYVRKARVSOELKAKVHLGDLKSIISBAPG 60
 QY 61 KCVPAVAVIEGAVRSVKEITNSQFVENCCKVIOQLTLOEHKVMWNRTHLMDCSKIIHOR 120
 DB 61 KCVPAVAVIEGAVRSVKEITNSQFVENCCKVIOQLTLOEHKVMWNRTHLMDCSKIIHOR 120
 QY 121 TMTVPFDLVPHEDGDVAVRVLPKPLDSVDLGLETVEYERKHPISQFTDVIIGHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGDVAVRVLPKPLDSVDLGLETVEYERKHPISQFTDVIIGHYISGERPK 180
 QY 181 GIQTEBMLKVGATLTGVELVDNNSVRLQPPKQGMQYISSLQPDSDLQOESSVRILM 240
 DB 181 GIQTEBMLKVGATLTGVELVDNNSVRLQPPKQGMQYISSLQPDSDLQOESSVRILM 240
 QY 241 KYLALVFGFATCATLFFILRKQYLOEROERLRLKQOEFOEHAQLLSRAKPEDRESLKS 300
 DB 241 KYLALVFGFATCATLFFILRKQYLOEROERLRLKQOEFOEHAQLLSRAKPEDRESLKS 300
 XX

DB 241 KYLALVFGFATCATLFTILRKQYLQROERLRLKQWEEFQHEAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSFKSCVFLGCGHVCSTCECYRALPEPKKCPICRAITRVIPLYNS 352
 DB 301 ACVCLSSFKSCVFLGCGHVCSTCECYRALPEPKKCPICRAITRVIPLYNS 352

RESULT 13
 ADU02286
 ID ADU02286 standard; protein; 511 AA.
 AC ADU02286;
 XX
 DT 27-JAN-2005 (first entry)
 DE Novel human polypeptide seqid 753.
 XX
 KW cytostatic; antipsoriatic; antiinflammatory; gene therapy; Nanodisc;
 KW proliferative disorder; inflammatory disorder; immune disorder;
 KW metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis;
 KW ulcerative colitis; human.
 OS Homo sapiens.
 EN WO2004093804-A2.
 PD 04-NOV-2004.
 PF 19-APR-2004; 2004WO-US012047.
 XX
 PR 18-APR-2003; 2003US-0463708P.
 PR 18-APR-2003; 2003US-0463732P.
 PR 02-MAY-2003; 2003US-0467199P.
 PR 19-MAY-2003; 2003US-0467230P.
 PR 19-MAY-2003; 2003US-0471306P.
 PR 08-JUL-2003; 2003US-0471336P.
 PR 08-JUL-2003; 2003US-0485223P.
 PR 14-JUL-2003; 2003US-0485224P.
 PR 14-JUL-2003; 2003US-048646P.
 PR 08-AUG-2003; 2003US-0493573P.
 PR 08-AUG-2003; 2003US-0493577P.
 PR 08-SEP-2003; 2003US-0505059P.
 XX
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
 XX
 PI Lee E, Hestir K, Chu K, Masuoka L, Williams LT;
 XX N-PSDB; ADU01554.
 DR WPI; 2004-775861/76.
 DR N-PSDB; ADU01554.
 PT New first nucleic acid molecule comprising a polynucleotide sequence
 PT given in the specification, useful in preparing a composition for
 PT diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
 XX
 PS Claim 14; SEQ ID NO 753; 291bp; English.
 XX
 CC The invention describes a new first nucleic acid molecule comprising a
 CC polynucleotide sequence given in the specification. Also described are:
 CC an animal injected with the nucleic acid molecule; a second nucleic acid
 CC molecule comprising a second polynucleotide sequence that is at least
 CC about 70, 80, 90 or 95% homologous to the first nucleic acid molecule or
 CC that hybridises to the first polynucleotide sequence under high
 CC stringency conditions; a vector comprising the nucleic acid molecule and
 CC a promoter that drives the expression of the nucleic acid molecule; a
 CC host cell transfected; a nucleic acid composition comprising a carrier or
 CC a buffer and one or more compositions comprising the nucleic acid
 CC molecule, vector or host cell; a substantially purified polypeptide; an
 CC animal injected with the polypeptide; a polypeptide composition
 CC comprising the polypeptide molecule and a carrier or buffer; a cell
 CC culture medium comprising the polypeptide or transfected cells
 CC transfected with the polynucleotide; making a transformed, transfected,

transduced, or infected host cell; synthesising Nanodiscs simultaneously
 and for synthesising a series of simultaneously-synthesised Nanodiscs
 sequentially utilising a dynamic system; preparing a hydrophobic protein
 for determination of crystal structure; immunising a non-human animal;
 screening for modulators of hydrophobic protein activity; a diagnostic
 kit; determining the presence of the nucleic acid molecule or its
 complement; determining the presence of an antibody to the polypeptide in
 a sample; an antibody specifically recognising, binding to or modulating
 the biological activity of at least one polypeptide encoded by a nucleic
 acid molecule or its biologically active fragment; an antibody
 composition comprising the antibody and a carrier; a bacteriophage, where
 the antibody is displayed on the bacteriophage; a bacterial cell
 comprising the bacteriophage; a non-human animal injected with the
 antibody; diagnosing a disease, disorder, syndrome, or condition
 comprising cancer, or proliferative, inflammatory, immune, metabolic,
 bone, CNS, genetic, bacterial and viral diseases, disorders, syndromes or
 conditions in a patient; a modulator composition comprising a modulator
 and a carrier; gene therapy; prophylactic or therapeutic treatment of a
 subject; an isolated modified cell comprising at least one first
 heterologous nucleic acid molecule, where the first heterologous nucleic
 acid molecule comprises a first polynucleotide sequence that encodes a
 first polypeptide; a non-human animal deficient in the polypeptide or
 CC that over-expresses the polypeptide; isolated tissues derived from the
 CC non-human animal; and one or more cells derived from the non-human
 CC animal. The nucleic acid is useful in preparing a composition for
 CC diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
 CC This is the amino acid sequence of a novel human polypeptide of the
 CC invention.

Sequence 511 AA;
 SQ

Query Match 98.0%; Score 1795; DB 8; Length 511;
 Best Local Similarity 100.0%; Pred. No. 7.6e-165;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSGRPSICPITLIGTTSVTAALYSYRQKARYSGLKAKYHIGEDIKSLISEAPG 60
 DB 1 MESSGRPSICPITLIGTTSVTAALYSYRQKARYSGLKAKYHIGEDIKSLISEAPG 60
 QY 61 KCVPAVIEGAVRSYKELTNSQFVENCQVILQRLTQEHKVMWNTTHLAMDCKIIR 120
 DB 61 KCVPAVIEGAVRSYKELTNSQFVENCQVILQRLTQEHKVMWNTTHLAMDCKIIR 120
 QY 121 TMTVPFDLVPHEDGDVAVRLKPLDSYDLGLFTYKFKHPSISQFTDVIHYISGERPK 180
 DB 121 TMTVPFDLVPHEDGDVAVRLKPLDSYDLGLFTYKFKHPSISQFTDVIHYISGERPK 180
 QY 181 GIOETEMLKVGATLTGGLVLDNNSVRLQPPKQMOYUYSQDPBSILQROESSVRLW 240
 DB 181 GIOETEMLKVGATLTGGLVLDNNSVRLQPPKQMOYUYSQDPBSILQROESSVRLW 240
 QY 241 KYLALVFGFATCATLFTILRKQYLQROERLRLKQWEEFQHEAQLLSRAKPEDRESLKS 300
 DB 241 KYLALVFGFATCATLFTILRKQYLQROERLRLKQWEEFQHEAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSFKSCVFLGCGHVCSTCECYRALPEPKKCPICRAITRVIPLYNS 345
 DB 301 ACVCLSSFKSCVFLGCGHVCSTCECYRALPEPKKCPICRAITRVIPLYNS 345

RESULT 14
 ABJ38698
 ID ABJ38698 standard; protein; 263 AA.
 AC ABJ38698;
 XX
 DT 04-AUG-2003 (first entry)
 DE Human nucleic acid-associated protein (NAAP) #28.
 XX
 KW Human, gene therapy; nucleic acid-associated protein; NAAP;
 KW cell proliferative disorder; cancer; neurological disorder; epilepsy;

KM immune disorder; inflammatory disorder; AIDS; allergy;
 KM developmental disorder; Cushing's syndrome.
 OS Homo sapiens.
 XX WO2003010329-A2.
 PD 06-FEB-2003.
 XX 25-JUL-2002; 2002MO-US023756.
 PF 26-JUL-2001; 2001US-0308189P.
 XX 27-JUL-2001; 2001US-0308171P.
 PR 02-AUG-2001; 2001US-0310139P.
 PR 03-AUG-2001; 2001US-0309974P.
 PR 08-AUG-2001; 2001US-0311072P.
 PR 10-AUG-2001; 2001US-0311642P.
 PR 10-AUG-2001; 2001US-0311717P.
 PR 12-OCT-2001; 2001US-0329688P.
 XX (INCY-) INCYTE GENOMICS INC.
 PA Tang YT, Nguyen DB, Yao MG, Warren BA, Griffin JA, Ison CH;
 PI Forsythe IJ, Becha SD, Yue H, Emerling BW, Walla NK, Richardson TW;
 PI Lee EA, Ramkumar J, Elliott VS, He A, Li JX, Hafalia AJA, Yang J;
 PI Santanala MM, Xu Y, Arvizu CS, Gandhi AR, Borowsky MD, Tran UK;
 PI Burford N, Sprague MW, Baughn MR, Swarnakar A, Policky JL, Lee SY;
 PI Jiang X, Jackson A, Chang H;
 XX WPI; 2003-248084/24.
 DR N-PSDB; ABR42547.
 XX New human nucleic acid associated proteins (NAAP), useful for diagnosing,
 PT treating and preventing diseases or conditions associated with the
 PT aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
 PT infections.
 CC Claim 1; Page 229; 263pp; English.
 CC The invention comprises the amino acid and coding sequences of human
 CC nucleic acid-associated proteins (NAAP). The DNA and protein sequences of
 CC the invention are useful for diagnosing, treating and preventing diseases
 CC or conditions associated with the decreased expression or overexpression
 CC of NAAP, such as: cell proliferative disorders (e.g. cancer);
 CC neurological disorders (e.g. epilepsy); immune/inflammatory disorders
 CC (e.g. AIDS and allergies); and developmental disorders (e.g. Cushing's
 CC syndrome). The present amino acid sequence represents a human nucleic
 CC acid-associated protein of the invention
 XX
 SQ Sequence 263 AA;
 Query Match 72.6%; Score 1328.5; DB 6; Length 263;
 Best Local Similarity 74.7%; Pred. No. 5,4e-120;
 Matches 263; Conservative 0; Mismatches 0; Indels 89; Gaps 1;
 QY 1 MESSGRPSICQILIGTTSVTAALYSVRQKARVSQELKAKKHLGSDLSISEARG 60
 DB 1 MESSGRPSICQFILIG----- 16
 QY 61 KCVPAVIEGAVRSVKEITNSQFVENCKGIQRLTQEHKMWNRITTHLMNDSKIIHOR 120
 DB 17 -----TTHLMNDSKIIHOR 31
 QY 121 TTTVPFDLVPHEDGVDAVAVLKPLDSVDLGLFTYEKHPISQSTTDVYIGYISGERPK 180
 DB 32 TTTVPFDLVPHEDGVDAVAVRKPLDSVDLGLFTYEKHPISQSTTDVYIGYISGERPK 91
 QY 181 GIOETREEMKVGATLTGVELVLDNNSVRLQPPKQMOYVLSQPPDSLLQOESSVRIM 240
 DB 92 GIOETREEMKVGATLTGVELVLDNNSVRLQPPKQMOYVLSQPPDSLLQOESSVRIM 151
 QY 241 KYIALVFGFATCATLFFILRKQYLOREELRLKOMQEFQHEHAQLLSRAKPEDRESLKS 300

DB 152 KYIALVFGFATCATLFFILRKQYLOREELRLKOMQEFQHEHAQLLSRAKPEDRESLKS 211
 QY 301 ACWCILSFKSCVFLFEGHVCSCTECYALPEPKKPCICROAIRVIPLYS 352
 DB 212 ACWCILSFKSCVFLFEGHVCSCTECYALPEPKKPCICROAIRVIPLYS 263
 RESULT 15
 AAU16309
 ID AAU16309 standard; protein, 174 AA.
 XX AAU16309;
 AC 07-NOV-2001 (first entry)
 DT Human novel secreted protein, Seq ID 1262.
 XX Human, immunosuppressive; antiarthritic; antirheumatic; cytostatic;
 KW cardiact; vasotropic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; vulnery;
 KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
 KW cerebral ischaemia; angiodenesis; nervous system disorder;
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;
 KW wound healing; epithelial cell proliferation; skin ageing; food additive;
 KW preservative; antiproliferative.
 XX Homo sapiens.
 OS WO200155322-A2.
 XX 02-AUG-2001.
 PD 17-JAN-2001; 2001WO-US001341.
 PF 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 14-AUG-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226881P.
 PR 22-AUG-2000; 2000US-0226882P.
 PR 22-AUG-2000; 2000US-0227183P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.

Db	61	LMKVLAIVRGFATCATLFFILRKQYLQROERLRLKQMOEFOEHEAQLLSRAKPEDXESL	120
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Db	121	KSACTVCLSSFKSCVPLECGHVCSTECYRALPEPKCPICROAITRVIPLYN	174

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